

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

File copy

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/12, 15/56, 9/26, C07K 14/47, 14/705, 14/785, A61K 38/17, 38/47		A2	(11) International Publication Number: WO 00/18922
			(43) International Publication Date: 6 April 2000 (06.04.00)
(21) International Application Number: PCT/US99/22685		(71) Applicant (for all designated States except US): INCYTE PHARMACEUTICALS, INC. [US/US]; 3174 Porter Drive, Palo Alto, CA 94304 (US).	
(22) International Filing Date: 29 September 1999 (29.09.99)		(72) Inventors; and	
(30) Priority Data:		(75) Inventors/Applicants (for US only): AU-YOUNG, Janice [US/US]; 1419 Kains Avenue, Berkeley, CA 94702 (US). LAL, Preeti [IN/US]; 2382 Lass Drive, Santa Clara, CA 95054 (US). BANDMAN, Olga [US/US]; 366 Anna Avenue, Mountain View, CA 94043 (US). REDDY, Roopa [IN/US]; 1233 W. McKinley Drive, Sunnyvale, CA 94086 (US). BAUGHN, Mariah, R. [US/US]; 14244 Santiago Road, San Leandro, CA 94577 (US). YUE, Henry [US/US]; 826 Lois Avenue, Sunnyvale, CA 94087 (US). HILLMAN, Jennifer, L. [US/US]; 230 Monroe Drive #12, Mountain View, CA 94040 (US).	
60/155,267 1 October 1998 (01.10.98) US 60/155,266 6 October 1998 (06.10.98) US 60/155,227 13 November 1998 (13.11.98) US 09/205,656 3 December 1998 (03.12.98) US Not furnished 3 December 1998 (03.12.98) US		(74) Agents: BILLINGS, Lucy, J. et al.; Incyte Pharmaceuticals, Inc., 3174 Porter Drive, Palo Alto, CA 94304 (US).	
(63) Related by Continuation (CON) or Continuation-in-Part (CIP) to Earlier Applications		(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
US 09/167,179 (CIP) Filed on 6 October 1998 (06.10.98) US 09/191,838 (CIP) Filed on 13 November 1998 (13.11.98) US 09/205,656 (CIP) Filed on 3 December 1998 (03.12.98) US 09/164,785 (CIP) Filed on 1 October 1998 (01.10.98)		Published Without international search report and to be republished upon receipt of that report.	

(54) Title: HUMAN CARBOHYDRATE-ASSOCIATED PROTEINS

```

1  M-----AGSYADSNAAVVK 714029
1  M LSLNNLQNI IYNPVI FV G T I P D J Q L D P G T GI 2810994

14  L D-----D G H L N N S L S S P Y Q A D 714029
31  L I V I R G H V P S D A D R F Q V D L Q N G S S V K P R A D GI 2810994

31  V Y F-----714029
61  V A L H F N P R F K R A G C I V C N T L I N E K W G R E E I GI 2810994

34  -----714029
91  T Y D T P F K R E K S F E I V I M V L K D K P Q V A V N G K GI 2810994

34  -----714029
121 H T L L Y G H R I G P E K I D T L G I Y G K V N I H S I G F GI 2810994

34  -----P 714029
151 S F S S D L Q S T Q A S S L E L T E I V R E N V P K S G T E GI 2810994

35  R L I V P F C G H I K G G M R P G K K V L V M G I V D L N F 714029
181 Q L S L F F A A R L N T P M G P G R T V V V Q G E V N A N A GI 2810994

65  E S P A I S L T C G D S E D P P A D V A I E L K A V E T D R 714029
211 K S F N V D L L A G K S R D-----I A L H L N P R L N I X GI 2810994

```

(57) Abstract

The invention provides human carbohydrate-associated proteins (CRBAP) and polynucleotides which identify and encode CRBAP. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with expression of CRBAP.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republic of Korea	PT	Portugal		
CN	China	KZ	Kazakhstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

HUMAN CARBOHYDRATE-ASSOCIATED PROTEINS

TECHNICAL FIELD

This invention relates to nucleic acid and amino acid sequences of human carbohydrate-associated proteins and to the use of these sequences in the diagnosis, treatment, and prevention of autoimmune/ inflammatory disorders, gastrointestinal disorders, infectious disorders, reproductive disorders, neurological disorders, eye disorders, and cell proliferative disorders, including cancer.

BACKGROUND OF THE INVENTION

Proteins are associated with carbohydrates in several ways. Glycoproteins have covalently attached carbohydrates which have been added to the proteins as they traverse the secretory pathway. Some proteins noncovalently associate with carbohydrate-containing macromolecules for purposes of binding, modifying, or degrading the carbohydrates. Carbohydrate-containing macromolecules, which include glycoproteins, glycolipids, glycosaminoglycans, and proteoglycans, are found on the cell surface and in the extracellular matrix. Glycosaminoglycans (GAGs) are linear unbranched polysaccharides composed of repetitive disaccharide units. GAGs exist free or as part of proteoglycans, large molecules composed of a core protein attached to one or more GAGs. (See Lodish, H. et al. (1995) Molecular Cell Biology, Scientific American Books, New York NY, pp. 1136-1142.)

Cell surface carbohydrate-containing macromolecules, including glycoproteins, glycolipids, and transmembrane proteoglycans, mediate adhesion with other cells and with components of the extracellular matrix. The extracellular matrix is comprised of diverse glycoproteins, GAGs, and carbohydrate-binding proteins which are secreted from the cell and assembled into an organized meshwork in close association with the cell surface. The interaction of the cell with the surrounding matrix profoundly influences cell shape, strength, flexibility, motility, and adhesion. These dynamic properties are intimately associated with signal transduction pathways controlling cell proliferation and differentiation, tissue construction, and embryonic development.

The GAG hyaluronan (HA) is found in the extracellular matrix of many cells, especially in soft connective tissues, and is abundant in synovial fluid. (Pitsillides, A.A. et al. (1993) *Int. J. Exp. Pathol.* 74:27-34.) HA seems to play important roles in cell regulation, development, and differentiation (Laurent, T.C. and Fraser, J.R. (1992) *FASEB J.* 6:2397-2404). HA functions in water and plasma protein homeostasis (Laurent, supra). HA may play a role in mitosis as its production increases in proliferating cells. HA is known to induce tumor cell adhesion and migration, and its small fragments are angiogenic. HA has been chemically modified as a

biomaterial for medical applications such as controlled drug release matrices, nerve guides, and wound dressings (Zhong, S.P. et al. (1994) *Biomaterials* 15:359-365). HA's tissue protective and rheological properties have proved useful in ophthalmic surgery. Serum HA is diagnostic of liver disease and various inflammatory conditions, such as rheumatoid arthritis. Interstitial edema caused by accumulation of HA may cause dysfunction in various organs (Laurent, *supra*).

Hyaluronidase is an enzyme that degrades HA to oligosaccharides by catalyzing the random hydrolysis of 1,4-linkages between N-acetyl-beta-D-glucosamine and D-glucuronate residues. Hyaluronidases have been found in organisms as diverse as bacteria, insects, reptiles, and mammals, and may function in cell adhesion, infection, angiogenesis, and signal transduction.

PH-20, a protein expressed in the mammalian testis and present on the plasma membrane of mouse and human sperm, has hyaluronidase activity (Lin, Y. et al. (1994) *J. Cell Biol.* 125:1157-63). PH-20 enables sperm to penetrate the mammalian egg's outer layer, which consists of about 3,000 cumulus cells embedded in an extracellular matrix rich in HA. Penetration of this layer is an essential step in the fertilization process. PH-20 is also expressed in some tumor cells. Non-testicular mammalian hyaluronidases also exist. The HYAL1 hyaluronidase is expressed in human serum while the lysosomal hyaluronidase HYAL2 is expressed in many cells (Lepperdinger, G. et al. (1998) *J. Biol. Chem.* 273:22466-22470). HYAL2 may have a role in producing distinct HA fragments that can induce angiogenesis and the expression of enzymes involved in signal transduction pathways, such as nitric oxide synthase. A lysosomal-type hyaluronidase may degrade HA in lung fibroblasts in a cytokine-regulated process (Sampson, P.M. et al. (1992) *J. Clin. Invest.* 90:1492-1503).

The venom of numerous animals including various snakes, bees, hornets, stone fish, platypus, scorpions, and lizards contain hyaluronidase. Hyaluronidase from the white face hornet is an allergen which induces an IgE response in susceptible people (Lu, G. et al. (1995) *J. Biol. Chem.* 270:4457-4465). Venom hyaluronidase is thought to act as a "spreading factor", an aid in the diffusion of toxins. Researchers have found that lizard venom hyaluronidase promotes the spread of the hemorrhagic area in mice injected with hemorrhagic toxin (Tu, A.T. and Hendon, R.R. (1983) *Comp. Biochem. Physiol. B* 76:377-383). Clostridium perfringens hyaluronidase is important for the pathogenicity of this bacterium, which causes food poisoning and gas gangrene (Canard, B. et al. (1994) *Mol. Gen. Genet.* 243:215-224). The hyaluronidase destroys connective tissue in the host, allowing Clostridium perfringens to spread from the initial site of infection and to colonize and attack surrounding tissue.

Hyaluronidases are associated with reproduction, cancer, and inflammation. Effective contraception (100%) was obtained in male and female guinea pigs immunized with PH-20

(Primakoff, P. et al. (1988) Nature 335:543-546). Based on these results researchers are continuing efforts to make an anti-sperm PH-20 contraceptive vaccine suitable for humans (Zhu, X. and Naz, R.K. (1994) Arch. Androl. 33:141-144). Hyaluronidase activity is significantly elevated in prostate tumor tissue compared to that in both normal prostate and benign prostate hyperplasia (Lokeshwar, V.B. et al. (1996) Cancer Res. 56:651-657). Furthermore, hyaluronidase levels in tissues correlate well with tumor progression. The combined therapy of hyaluronidase, vindesine, cisplatin, and radiation is highly effective against advanced squamous cell cancer of the head and neck and is well tolerated by most human patients (Klocker, J. et al. (1995) Am. J. Clin. Oncol. 18:425-428). Hyaluronidase in combination with the chemotherapeutic drug vinblastine had significant antitumor effects on SK-Mel-3 melanoma cells implanted in nude mice (Spruss, T. et al. (1995) J. Cancer Res. Clin. Oncol. 121:193-202). Furthermore, hyaluronidase was well tolerated in test animals and prevented the local inflammation reactions that are commonly seen after subcutaneous vinblastine injections.

15 N-Acetylglucosamine Receptor

Many secreted proteins and integral membrane proteins have oligosaccharide chains attached by *O*- or *N*-glycosidic linkage. *N*-linked oligosaccharides contain a common pentasaccharide consisting of three mannose and two N-acetylglucosamine residues. Additional sugars are often attached to this common backbone, either as additional mannose residues or as a complex array of N-acetylglucosamine, galactose, sialic acid, and L-fucose. A large number of surface sugar patterns are possible, thereby providing a large amount of information that may be of functional importance.

Lectins are carbohydrate-binding proteins, originally described in plants, that interpret the information provided by oligosaccharide moieties. The liver cell asialoglycoprotein receptor is a lectin that recognizes sialic acid residues. Immunoglobulins and peptide hormones, which contain terminal sialic acid residues, are removed from the blood after they bind to the liver receptor and are transported into liver cells by endocytosis. Selectins are cell surface receptors on neutrophils and other leukocytes that bind carbohydrate moieties on lymph node tissue, endothelium, and activated platelets. The selectins target leukocytes to sites of injury during an inflammatory response. Cell surface carbohydrates also appear to act as guides in neuronal outgrowth.

N-acetylglucosamine (GlcNAc)-binding proteins have been described in several cell types and are involved in a variety of functions. The chicken hepatic lectin (CHL) appears to be the avian homolog of the mammalian asialoglycoprotein receptor, but with a greater affinity for GlcNAc instead of sialic acid. CHL is a homotrimer in the plasma membrane of chicken liver cells and it

mediates the clearance of serum glycoproteins that have a terminal GlcNAc residue. The ability of ligand to bind to CHL requires Ca^{2+} , which is also the case with other Ca^{2+} -dependent (C-type) lectins such as asialoglycoprotein, mannose-binding protein (MBP), and selectin cell adhesion molecules. (Burrows, L. et al (1997) *Biochem. J.* 324:673-680.)

5 GlcNAc-binding proteins have been identified in the nucleus of human myeloid leukemia cells. These lectins bind to O-linked GlcNAc, present on nuclear glycoproteins. Interaction between lectins and nuclear glycoproteins inhibit trafficking of molecules between the nucleus and cytoplasm, and inhibit transcriptional activation by the transcription factor Sp1. (Felin, M. et al (1994) *J. Cell. Biochem.* 56:527-535.)

10 GlcNAc-binding protein also regulates trafficking of thyroglobin in the thyroid. Thyroglobin, the precursor of the thyroid hormones, is stored in the thyroid follicles as a prohormone. Production of the prohormone includes addition of a carbohydrate moiety as it passes through the ER and Golgi, and iodination of tyrosine residues in exocytic vesicles. Complete maturation of prohormone takes 24-36 hours and requires successive recycling through the
15 iodination steps. Stimulation of the thyroid with thyroid stimulating hormone (TSH) causes follicular cells to take up thyroglobin from the follicular lumen by pinocytosis. The prohormone moves into an endosomal compartment, where immature thyroglobin is picked up by an endosomal receptor and passed back to the thyroperoxidase iodination site via the Golgi. Only mature prohormone is passed to the lysosome for degradation, which produces the thyroid hormones
20 thyroxine (T_4) and triiodothyronine (T_3). The thyroglobin domain on the immature prohormone interacts with the endosomal receptor through N-acetylglucosamine (GlcNAc) residues. The domain also includes tyrosyl residues involved in iodination and hormonogenesis. The thyroglobin receptor is an endogenous lectin showing specificity for N-acetylglucosamine moieties. (Mezgrhani, H. et al. (1997) *J. Biol. Chem.* 272:23340-23346.)

25 Regulation of levels of circulating thyroid hormone and glycosylated immunoglobulins is important for proper embryonic and fetal development and maintains metabolic activity. Thyroid hormones regulate metabolic rate. They increase metabolism by increasing the rate of carbohydrate absorption in the intestine, regulating lipid metabolism, and increasing mitochondrial respiration and oxidative phosphorylation. Thyroid hormones also influence body growth and nervous system
30 development in the fetus. Increases in the level of circulating IgG with terminal GlcNAc residues appears to be associated with rheumatoid arthritis, Crohn's disease, and Sjogren's syndrome. (Bond, A. et al. (1997) *J. Autoimmun.* 10:77-85.)

Olfactomedin Family Proteins

The glycoprotein olfactomedin is a major component of the extracellular mucous matrix secreted by olfactory epithelial cells (Snyder, D. A. et al. (1991) *Biochemistry* 30:9143-9153; Yokoe, H. and Anholt, R. R. H. (1993) *Proc. Natl. Acad. Sci. USA* 90:4655-4659). In vivo, olfactomedin exists as a homodimer, the subunits of which are joined by intermolecular disulfide bonds and carbohydrate interactions. Olfactomedin may contribute to the protective and lubricating functions of mucous and/or promote the interaction of odorants and olfactory receptors in the nasal tract.

The recent identification of several proteins with similarity to olfactomedin suggests that olfactomedin and related proteins may define a distinct family of extracellular matrix glycoproteins. Two glycoprotein isoforms, designated neuronal olfactomedin-related glycoprotein-AMZ (NORG-AMZ) and -BMZ (NORG-BMZ), have been identified in rat brain (Danielson, P. E. et al. (1994) *J. Neurosci. Res.* 38:468-478). The carboxy-terminal 175 amino acids of both NORG-AMZ and NORG-BMZ share 33% amino acid identity and 19% conservative amino acid substitutions with the C-terminal region of olfactomedin. The mRNAs encoding NORG-AMZ and NORG-BMZ are transcribed from alternative promoters of a single gene and differ in their 5' ends. In situ hybridization and Northern analysis indicate that the mRNAs are expressed exclusively in the brain, particularly in neurons of the cortex and the hippocampus. Both NORG-AMZ and NORG-BMZ are predicted to contain signal peptides at their N-termini, suggesting that these proteins are both secreted. In addition, homologs of these proteins have also been discovered in mice which are virtually identical to the rat proteins (Nagano, T. et al. (1998) *Brain Res. Mol. Brain Res.* 53:13-23).

Another olfactomedin-related protein has been implicated in the development of primary open angle glaucoma (POAG) (Fingert, J. H. et al. (1998) *Genome Res.* 8:377-384). POAG is the most prevalent form of glaucoma, a disease which may cause irreversible blindness if left untreated. In the United States alone, glaucoma affects about 2.3 million people and blinds about 12,000 per year. POAG is characterized by progressive degeneration and cupping of the optic nerve, loss of peripheral visual field, and increased intraocular pressure. The development of both acquired and inherited forms of POAG is correlated with the presence of mutations in the *GLC1A* gene. Non-disease-causing polymorphisms have also been identified in *GLC1A*. *GLC1A* has been cloned from humans and mice and encodes a protein called myocilin. The C-terminal 250 amino acids of human myocilin shares 35% identity with the C-terminal region of olfactomedin. *GLC1A* is expressed in the eye, particularly in the ciliary body, retina, iris, and trabecular meshwork. *GLC1A* is also expressed in a variety of other tissues including the heart, skeletal muscle, stomach, thyroid, trachea, bone marrow, thymus, prostate, small intestine, and colon. *GLC1A* expression was not detected in brain, placenta, liver, kidney, spleen, or leukocytes.

Lectins

Lectins comprise a ubiquitous family of extracellular glycoproteins which bind cell surface carbohydrates specifically and reversibly, resulting in the agglutination of cells. (Reviewed in Drickamer, K. and Taylor, M. E. (1993) *Annu. Rev. Cell Biol.* 9:237-264.) This function is particularly important for activation of the immune response. Lectins mediate the agglutination and mitogenic stimulation of lymphocytes at sites of inflammation (Lasky, L. A. (1991) *J. Cell. Biochem.* 45:139-146; Paietta, E. et al. (1989) *J. Immunol.* 143:2850-2857).

Animal lectins have been grouped into four distinct families: 1) C-type lectins, which include selectins; 2) P-type lectins; 3) galectins (formerly termed S-type lectins or S-Lac lectins); and 4) pentraxins (Barondes, S.H. et al. (1994) *J. Biol. Chem.* 269:20807-20810). The C-type lectins bind carbohydrate ligands in a Ca^{2+} -dependent manner and are structurally related to the asialoglycoprotein receptor. Selectins, a subcategory of the C-type lectins, are composite transmembrane molecules which are involved in cell-cell interactions. The selectins include lymphocyte homing receptors and platelet/endothelial cell surface receptors (Stoolman, L.M. (1989) *Cell* 56:907-910).

C-type lectins contain Ca^{2+} -dependent carbohydrate-recognition domains. While prototypical C-type lectins are integral membrane proteins (e.g., the asialoglycoprotein receptor), a number of soluble C-type lectins have been identified. Examples of C-type lectins include pulmonary surfactant proteins A and D (SP-A and SP-D), mammalian Clq protein, bovine collectin-43, bovine conglutinin, mouse intelectin, and mannose-binding protein.

SP-D is a member of a family of host defense lectins, designated collectins. Collectins function in innate immunity in the lung and circulatory system to protect against a wide variety of potential pathogens, including viruses, bacteria, and fungi (Reid, K.B. (1998) *Immunobiology*, 199:200-207). Collectins have a collagen-like N-terminus domain which includes a number of Gly-Xaa-Xaa repeat,; an internal region termed the neck region, and a carbohydrate-binding C-terminus domain. SP-D is synthesized only in the lung (Lim et al. (1993) *Immunology*, 78:159-165). SP-D inhibits lectin- and anti-CD3-stimulated proliferation of human leukocytes *in vitro*, and this inhibition is associated with decreased cellular production of interleukin-2. (Borron, P.J. et al. (1998) *J. Immunol.* 161:4599-4603.)

Mouse intelectin is a homolog of the frog oocyte lectin and is expressed in the murine intestinal paneth cells of the small intestine. Frog oocyte lectin participates in the formation of the fertilization envelope and prevents polyspermy. Komiya et al. (1998, *Biochem. Biophys. Res. Comm.* 251:759-762) suggest that murine intelectin may be involved in host defense against microorganisms.

The galectin subfamily includes lectins that bind β -galactoside carbohydrate moieties in a thiol-dependent manner. (Reviewed in Hadari, Y. R. et al. (1995) *J. Biol. Chem.* 270:3447-3453.) Galectins are widely expressed and developmentally regulated. Because all galectins lack an N-terminal signal peptide, it is suggested that galectins are externalized through an atypical secretory mechanism. Two classes of galectins have been defined based on molecular weight and oligomerization properties. Small galectins form homodimers and are about 14 to 16 kilodaltons in mass, while large galectins are monomeric and about 29-37 kilodaltons. Galectins contain a characteristic carbohydrate recognition domain (CRD), also known as a galaptin domain. The CRD is about 140 amino acids long and contains several conserved residues. Secondary structure predictions indicate that the CRD forms several β -sheets. Known galectins contain one or two CRDs. (See Prosite PDOC00279 Vertebrate galactoside-binding lectin signature.)

Galectins play a number of roles in diseases and conditions associated with cell-cell and cell-matrix interactions. For example, certain galectins associate with sites of inflammation and bind to cell surface immunoglobulin E molecules. In addition, galectins may play an important role in cancer metastasis. Galectin overexpression is correlated with the metastatic potential of cancers in humans and mice. Moreover, anti-galectin antibodies inhibit processes associated with cell transformation, such as cell aggregation and anchorage-independent growth.

Galectin-8, also known as prostate carcinoma tumor antigen 1 (PCTA-1), is a novel galectin implicated in cancer progression (Su, Z.-Z. et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:7252-7257). Galectin-8 was initially identified as the cell surface antigen recognized by a prostate tumor-directed monoclonal antibody, Pro 1.5. The galectin-8 gene encodes a 317-amino acid protein which contains two CRDs. Galectin-8 is expressed in invasive prostate carcinomas and early-stage prostate cancers, but not in normal prostate or benign prostatic hypertrophic tissue. In addition, galectin-8 is shed from the surface of cultured prostate cancer cells into the growth media. Together, these results suggest that detection of galectin-8 may be useful for early diagnosis of prostate cancer and that levels of galectin-8 in the circulation may correlate with disease progression. In addition, preliminary studies in mice suggest that the monoclonal antibody Pro 1.5 may itself be an effective therapeutic agent against tumor progression.

The discovery of new human carbohydrate-associated proteins and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of autoimmune/ inflammatory disorders, gastrointestinal disorders, infectious disorders, reproductive disorders, neurological disorders, eye disorders, and cell proliferative disorders, including cancer.

SUMMARY OF THE INVENTION

The invention is based on the discovery of new human carbohydrate-associated proteins, referred to collectively as "CRBAP" and individually as "CRBAP-1," "CRBAP-2," "CRBAP-3," "CRBAP-4," "CRBAP-5," "CRBAP-6," and "CRBAP-7". In one aspect, the invention provides a
5 substantially purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-7, and fragments thereof.

The invention further provides a substantially purified variant having at least 90% amino acid sequence identity to the amino acid sequence of SEQ ID NO:1-7, and fragments thereof. The invention also provides an isolated and purified polynucleotide encoding the polypeptide comprising
10 the amino acid sequence of SEQ ID NO:1-7, and fragments thereof. The invention also includes an isolated and purified polynucleotide variant having at least 70% polynucleotide sequence identity to the polynucleotide encoding the polypeptide comprising the amino acid sequence of SEQ ID NO:1-7, and fragments thereof.

The invention further provides an isolated and purified polynucleotide which hybridizes
15 under stringent conditions to the polynucleotide encoding the polypeptide comprising the amino acid sequence of SEQ ID NO:1-7, or fragments thereof, as well as an isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide encoding the polypeptide comprising the amino acid sequence of SEQ ID NO:1-7, and fragments thereof.

The invention also provides a method for detecting a polynucleotide in a sample containing
20 nucleic acids, the method comprising the steps of (a) hybridizing the complement of the polynucleotide sequence to at least one of the polynucleotides of the sample, thereby forming a hybridization complex; and (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of a polynucleotide in the sample. In one aspect, the method further comprises amplifying the polynucleotide prior to hybridization.

25 The invention also provides an isolated and purified polynucleotide comprising the polynucleotide sequence of SEQ ID NO:8-14, and fragments thereof. The invention further provides an isolated and purified polynucleotide comprising the polynucleotide sequence of SEQ ID NO:8 which contains a single nucleotide polymorphism with C replacing T at position 428. The invention further provides an isolated and purified polynucleotide variant having at least 70% polynucleotide
30 sequence identity to the polynucleotide comprising the polynucleotide sequence of SEQ ID NO:8-14, and fragments thereof. The invention also provides an isolated and purified polynucleotide having a sequence complementary to the polynucleotide comprising the polynucleotide sequence of SEQ ID NO:8-14, and fragments thereof.

The invention further provides an expression vector containing at least a fragment of the

polynucleotide encoding the polypeptide comprising the sequence of SEQ ID NO:1-7, and fragments thereof. In another aspect, the expression vector is contained within a host cell.

The invention also provides a method for producing a polypeptide, the method comprising the steps of: (a) culturing the host cell containing an expression vector containing at least a fragment of a polynucleotide under conditions suitable for the expression of the polypeptide; and (b) recovering the polypeptide from the host cell culture.

The invention also provides a pharmaceutical composition comprising a substantially purified polypeptide having the sequence of SEQ ID NO:1-7, or fragments thereof in conjunction with a suitable pharmaceutical carrier.

The invention further includes a purified antibody which binds to a polypeptide comprising the sequence of SEQ ID NO:1-7, and fragments thereof, as well as a purified agonist and a purified antagonist of the polypeptide.

The invention also provides a method for treating or preventing a disorder associated with decreased expression or activity of CRBAP, the method comprising administering to a subject in need of such treatment an effective amount of a pharmaceutical composition comprising a substantially purified polypeptide having the amino acid sequence of SEQ ID NO:1-7, and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

The invention also provides a method for treating or preventing a disorder associated with increased expression or activity of CRBAP, the method comprising administering to a subject in need of such treatment an effective amount of an antagonist of the polypeptide having the amino acid sequence of SEQ ID NO:1-7, and fragments thereof.

BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figures 1A and 1B show the amino acid sequence alignment between CRBAP-1 (714029; SEQ ID NO:1) and human galactin-8 (GI 2810994; SEQ ID NO:15), produced using the multisequence alignment program of LASERGENE software (DNASTAR, Madison WI).

Figures 2A, 2B, 2C, 2D, and 2E show the amino acid sequence alignment between CRBAP-2 (1450775; SEQ ID NO:2) and Clostridium perfringens hyaluronidase (GI 144861; SEQ ID NO:16).

Figures 3A and 3 B show the amino acid sequence alignment between CRBAP-3 (3369350; SEQ ID NO:3) and human TGR-CL10C (GI 1247124; SEQ ID NO:17), produced using the multisequence alignment program of LASERGENE software (DNASTAR, Madison WI).

Figures 4A and 4B show the amino acid sequence alignment among residues 147 through 402 of CRBAP-4 (1648214; SEQ ID NO:4), residues 159 through 409 of CRBAP-5 (2743295; SEQ

ID NO:5), and residues 204 through 457 of rat NORG-AMZ (GI 442368; SEQ ID NO:18), produced using the multisequence alignment program of LASERGENE software (DNASTAR, Madison WI).

Figures 5A and 5B show the amino acid sequence alignment between CRBAP-6 (2821011; SEQ ID NO:6) and bovine pulmonary SP-D (GI 415939; SEQ ID NO:19), produced using the
5 multisequence alignment program of LASERGENE software (DNASTAR, Madison WI).

Figures 6A and 6B show the amino acid sequence alignment between CRBAP-7 (2921920; SEQ ID NO:7) and murine intelectin (GI 3357909; SEQ ID NO:20), produced using the multisequence alignment program of LASERGENE software.

Table 1 shows nucleotide and polypeptide sequence identification numbers (SEQ ID NO),
10 clone identification numbers (clone ID), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding CRBAP.

Table 2 shows features of each polypeptide sequence including potential motifs, homologous sequences, and methods and algorithms used for identification of CRBAP.

Table 3 shows the tissue-specific expression patterns of each nucleic acid sequence as
15 determined by northern analysis, diseases or disorders associated with these tissues, and the vector into which each cDNA was cloned.

Table 4 describes the tissues used to construct the cDNA libraries from which Incyte cDNA clones encoding CRBAP were isolated.

Table 5 shows the tools, programs, and algorithms used to analyze CRBAP along with
20 applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is understood that this invention is not limited to the particular machines, materials and methods
25 described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a," "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a
30 reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention

belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the publications and which might be used in connection with the invention. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

"CRBAP" refers to the amino acid sequences of substantially purified CRBAP obtained from any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine, and preferably the human species, from any source, whether natural, synthetic, semi-synthetic, or recombinant.

The term "agonist" refers to a molecule which, when bound to CRBAP, increases or prolongs the duration of the effect of CRBAP. Agonists may include proteins, nucleic acids, carbohydrates, or any other molecules which bind to and modulate the effect of CRBAP.

An "allelic variant" is an alternative form of the gene encoding CRBAP. Allelic variants may result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. Any given natural or recombinant gene may have none, one, or many allelic forms. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

"Altered" nucleic acid sequences encoding CRBAP include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as CRBAP or a polypeptide with at least one functional characteristic of CRBAP. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe of the polynucleotide encoding CRBAP, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding CRBAP. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent CRBAP. Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of CRBAP is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, positively charged

amino acids may include lysine and arginine, and amino acids with uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine, and valine; glycine and alanine; asparagine and glutamine; serine and threonine; and phenylalanine and tyrosine.

The terms "amino acid" or "amino acid sequence" refer to an oligopeptide, peptide, polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. In this context, "fragments," "immunogenic fragments," or "antigenic fragments" refer to fragments of CRBAP which are preferably at least 5 to about 15 amino acids in length, most preferably at least 14 amino acids, and which retain some biological activity or immunological activity of CRBAP. Where "amino acid sequence" is recited to refer to an amino acid sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence. Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which, when bound to CRBAP, decreases the amount or the duration of the effect of the biological or immunological activity of CRBAP. Antagonists may include proteins, nucleic acids, carbohydrates, antibodies, or any other molecules which decrease the effect of CRBAP.

The term "antibody" refers to intact molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind CRBAP polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

The term "antigenic determinant" refers to that fragment of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (given regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

The term "antisense" refers to any composition containing a nucleic acid sequence which is

complementary to the "sense" strand of a specific nucleic acid sequence. Antisense molecules may be produced by any method including synthesis or transcription. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form duplexes and to block either transcription or translation. The designation "negative" can refer to the antisense strand, and the designation "positive" can refer to the sense strand.

The term "biologically active," refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" refers to the capability of the natural, recombinant, or synthetic CRBAP, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The terms "complementary" or "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence "5' A-G-T 3'" bonds to the complementary sequence "3' T-C-A 5'." Complementarity between two single-stranded molecules may be "partial," such that only some of the nucleic acids bind, or it may be "complete," such that total complementarity exists between the single stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands. This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands, and in the design and use of peptide nucleic acid (PNA) molecules.

A "composition comprising a given polynucleotide sequence" or a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding CRBAP or fragments of CRBAP may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been resequenced to resolve uncalled bases, extended using XL-PCR kit (Perkin-Elmer, Norwalk CT) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from the overlapping sequences of more than one Incyte Clone using a computer program for fragment assembly, such as the GELVIEW Fragment Assembly system (GCG, Madison WI). Some sequences have been both extended and assembled to produce the consensus sequence.

The term "correlates with expression of a polynucleotide" indicates that the detection of the

presence of nucleic acids, the same or related to a nucleic acid sequence encoding CRBAP, by northern analysis is indicative of the presence of nucleic acids encoding CRBAP in a sample, and thereby correlates with expression of the transcript from the polynucleotide encoding CRBAP.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the
5 absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to the chemical modification of a polypeptide sequence, or a polynucleotide sequence. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural
10 molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

The term "similarity" refers to a degree of complementarity. There may be partial similarity or complete similarity. The word "identity" may substitute for the word "similarity." A partially
15 complementary sequence that at least partially inhibits an identical sequence from hybridizing to a target nucleic acid is referred to as "substantially similar." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined using a hybridization assay (Southern or northern blot, solution hybridization, and the like) under conditions of reduced stringency. A substantially similar sequence or hybridization probe will compete for and inhibit the
20 binding of a completely similar (identical) sequence to the target sequence under conditions of reduced stringency. This is not to say that conditions of reduced stringency are such that non-specific binding is permitted, as reduced stringency conditions require that the binding of two sequences to one another be a specific (i.e., a selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of
25 complementarity (e.g., less than about 30% similarity or identity). In the absence of non-specific binding, the substantially similar sequence or probe will not hybridize to the second non-complementary target sequence.

The phrases "percent identity" or "% identity" refer to the percentage of sequence similarity found in a comparison of two or more amino acid or nucleic acid sequences. Percent identity can be
30 determined electronically, e.g., by using the MEGALIGN program (DNASTAR) which creates alignments between two or more sequences according to methods selected by the user, e.g., the clustal method. (See, e.g., Higgins, D.G. and P.M. Sharp (1988) Gene 73:237-244.) The clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. The percentage similarity between two amino acid

sequences, e.g., sequence A and sequence B, is calculated by dividing the length of sequence A, minus the number of gap residues in sequence A, minus the number of gap residues in sequence B, into the sum of the residue matches between sequence A and sequence B, times one hundred. Gaps of low or of no similarity between the two amino acid sequences are not included in determining percentage similarity. Percent identity between nucleic acid sequences can also be counted or calculated by other methods known in the art, e.g., the Jotun Hein method. (See, e.g., Hein, J. (1990) Methods Enzymol. 183:626-645.) Identity between sequences can also be determined by other methods known in the art, e.g., by varying hybridization conditions.

"Human artificial chromosomes" (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the elements required for stable mitotic chromosome segregation and maintenance.

The term "humanized antibody" refers to antibody molecules in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

"Hybridization" refers to any process by which a strand of nucleic acid binds with a complementary strand through base pairing.

The term "hybridization complex" refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C₀t or R₀t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words "insertion" or "addition" refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively, to the sequence found in the naturally occurring molecule.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

The term "microarray" refers to an arrangement of distinct polynucleotides on a substrate.

The terms "element" or "array element" in a microarray context, refer to hybridizable polynucleotides arranged on the surface of a substrate.

The term "modulate" refers to a change in the activity of CRBAP. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other

biological, functional, or immunological properties of CRBAP.

The phrases "nucleic acid" or "nucleic acid sequence," as used herein, refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material. In this context, "fragments" refers to those nucleic acid sequences which comprise a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:8-14, for example, as distinct from any other sequence in the same genome. For example, a fragment of SEQ ID NO:8-14 is useful in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:8-14 from related polynucleotide sequences. A fragment of SEQ ID NO:8-14 is at least about 15-20 nucleotides in length. The precise length of the fragment of SEQ ID NO:8-14 and the region of SEQ ID NO:8-14 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment. In some cases, a fragment, when translated, would produce polypeptides retaining some functional characteristic, e.g., antigenicity, or structural domain characteristic, e.g., ATP-binding site, of the full-length polypeptide.

The terms "operably associated" or "operably linked" refer to functionally related nucleic acid sequences. A promoter is operably associated or operably linked with a coding sequence if the promoter controls the translation of the encoded polypeptide. While operably associated or operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements, e.g., repressor genes, are not contiguously linked to the sequence encoding the polypeptide but still bind to operator sequences that control expression of the polypeptide.

The term "oligonucleotide" refers to a nucleic acid sequence of at least about 6 nucleotides to 60 nucleotides, preferably about 15 to 30 nucleotides, and most preferably about 20 to 25 nucleotides, which can be used in PCR amplification or in a hybridization assay or microarray. "Oligonucleotide" is substantially equivalent to the terms "amplimer," "primer," "oligomer," and "probe," as these terms are commonly defined in the art.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

The term "sample" is used in its broadest sense. A sample suspected of containing nucleic acids encoding CRBAP, or fragments thereof, or CRBAP itself, may comprise a bodily fluid; an

extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" or "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, or an antagonist. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

The term "stringent conditions" refers to conditions which permit hybridization between polynucleotides and the claimed polynucleotides. Stringent conditions can be defined by salt concentration, the concentration of organic solvent, e.g., formamide, temperature, and other conditions well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization temperature.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least about 60% free, preferably about 75% free, and most preferably about 90% free from other components with which they are naturally associated.

A "substitution" refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells, trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

"Transformation" describes a process by which exogenous DNA enters and changes a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for transformation is selected based on the type of host cell being transformed and may include, but is not limited to, viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for limited periods of time.

A "variant" of CRBAP polypeptides refers to an amino acid sequence that is altered by one or more amino acid residues. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties (e.g., replacement of leucine with isoleucine). More rarely, a variant may have "nonconservative" changes (e.g., replacement of glycine with tryptophan). Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE software (DNASTAR).

The term "variant," when used in the context of a polynucleotide sequence, may encompass a polynucleotide sequence related to CRBAP. This definition may also include, for example, "allelic" (as defined above), "splice," "species," or "polymorphic" variants. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or an absence of domains. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

THE INVENTION

The invention is based on the discovery of new human carbohydrate-associated proteins (CRBAP), the polynucleotides encoding CRBAP, and the use of these compositions for the diagnosis, treatment, or prevention of autoimmune/ inflammatory disorders, gastrointestinal disorders, infectious disorders, reproductive disorders, neurological disorders, eye disorders, and cell proliferative disorders, including cancer.

Table 1 lists the Incyte Clones used to derive full length nucleotide sequences encoding CRBAP. Columns 1 and 2 show the sequence identification numbers (SEQ ID NO) of the amino acid and nucleic acid sequences, respectively. Column 3 shows the clone ID of the Incyte Clone in which nucleic acids encoding each CRBAP were identified, and column 4 shows the cDNA libraries from which these clones were isolated. Column 5 shows Incyte clones, corresponding cDNA libraries, and shotgun sequences which are useful as fragments in hybridization technologies and are part of the consensus nucleotide sequence of each CRBAP.

The polynucleotide sequence encoding CRBAP-1 (SEQ ID NO:8) contains a single

nucleotide polymorphism with C replacing T at position 428. C was found at position 428 in 10% of the clones, while T was found at position 428 in 90% of the clones.

The columns of Table 2 show various properties of the polypeptides of the invention: column 1 references the SEQ ID NO; column 2 shows the number of amino acid residues in each polypeptide; column 3, potential phosphorylation sites; column 4, potential glycosylation sites; column 5, the amino acid residues comprising signature sequences and motifs; column 6, the identity of each protein; and column 7, analytical methods used to identify each protein through sequence homology and protein motifs.

PFAM analysis indicates that CRBAP-1 resembles vertebrate galactoside-binding lectins from G58 through D165. As shown in Figures 1A and 1B, CRBAP-1 has chemical and structural similarity with human galectin-8 (GI 2810994; SEQ ID NO:15). In particular, CRBAP-1 and human galectin-8 share 28% identity. CRBAP-1 and the first galactin domain of human galectin-8 (residues 1 through 153) share 23% identity. CRBAP-1 and the second galactin domain of human galectin-8 (residues 185 through 315) share 34% identity.

As shown in Figures 2A, 2B, 2C, 2D, and 2E, CRBAP-2 has chemical and structural similarity with Clostridium perfringens hyaluronidase (GI 144861; SEQ ID NO:16). In particular, CRBAP-2 and Clostridium perfringens hyaluronidase share 14% identity.

As shown in Figures 3A and 3B, CRBAP-3 has chemical and structural similarity with human TGR-CL10C (GI 1247124; SEQ ID NO:17). In particular, CRBAP-3 and human TGR-CL10C share 30% identity over the length of CRBAP-3. In addition, CRBAP-3 and TGR-CL10C share 100% identity from residue P128 through H220.

As shown in Figures 4A and 4B, the C-terminus of CRBAP-4 from G147 to K402 shares 25% amino acid sequence identity with the C-terminus of rat NORG-AMZ (GI 442368; SEQ ID NO:18) from G204 to L457. In particular, the potential phosphorylation sites at T268, T295, and S352 and the predicted signal peptide in CRBAP-4 are conserved in rat NORG-AMZ. In addition, the C-terminus of CRBAP-4 from G147 to K402 also shares 24% amino acid sequence identity with the C-terminus of myocilin (GI 3065679; sequence not shown). As also shown in Figures 4A and 4B, the C-terminus of CRBAP-5 from T159 to S409 shares 33% amino acid sequence identity with the C-terminus of rat NORG-AMZ from G204 to L457. In particular, the potential phosphorylation sites at S215, S277, and T381 in CRBAP-5 are conserved in rat NORG-AMZ.

As shown in Figures 5A and 5B, CRBAP-6 has chemical and structural similarity with bovine lung SP-D (GI 415939; SEQ ID NO:19). In particular, CRBAP-6 and bovine lung SP-D share 32% identity, the signal peptide sequence, the C-type lectin and the C1q domain protein sequences, four conserved cysteine residues at C170, C242, C256, and C264, and a collagen-like

domain.

As shown in Figures 6A and 6B, CRBAP-7 has chemical and structural similarity with murine intelectin (GI 3357909; SEQ ID NO:20). In particular, CRBAP-7 and murine intelectin share 79% identity, five potential casein kinase II phosphorylation sites, one potential protein kinase C phosphorylation site, and have similar isoelectric points of 8.1 and 7.8, respectively.

The columns of Table 3 show the tissue-specificity and disease-association of nucleotide sequences encoding CRBAP. The first column of Table 3 lists the polynucleotide sequence identifiers. The second column lists tissue categories which express CRBAP as a fraction of total tissue categories expressing CRBAP. The third column lists the disease classes associated with those tissues expressing CRBAP. The fourth column lists the vectors used to subclone the cDNA library. Of particular note is the expression of CRBAP-1 and CRBAP-2 in libraries associated with cancer and cell proliferation, inflammation and immune response, reproductive tissues, and nervous tissues. Also of particular note is the expression of CRBAP-3 in reproductive, nervous, gastrointestinal tissues, the expression of CRBAP-6 in liver, kidney, ovary, gut, adrenal gland, and secretory epithelium, and the expression of CRBAP-7 in small intestine with Crohn's disease, and with lung, ovary, testis, and secretory epithelium.

The invention also encompasses CRBAP variants. A preferred CRBAP variant is one which has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% amino acid sequence identity to the CRBAP amino acid sequence, and which contains at least one functional or structural characteristic of CRBAP.

The invention also encompasses polynucleotides which encode CRBAP. In a particular embodiment, the invention encompasses a polynucleotide sequence comprising the sequence of SEQ ID NO:8-14, which encodes CRBAP.

The invention also encompasses a variant of a polynucleotide sequence encoding CRBAP. In particular, such a variant polynucleotide sequence will have at least about 70%, more preferably at least about 85%, and most preferably at least about 95% polynucleotide sequence identity to the polynucleotide sequence encoding CRBAP. A particular aspect of the invention encompasses a variant of SEQ ID NO:8-14 which has at least about 70%, more preferably at least about 85%, and most preferably at least about 95% polynucleotide sequence identity to SEQ ID NO:8-14. Any one of the polynucleotide variants described above can encode an amino acid sequence which contains at least one functional or structural characteristic of CRBAP.

It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding CRBAP, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be

produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring CRBAP, and all such variations are to be considered
5 as being specifically disclosed.

Although nucleotide sequences which encode CRBAP and its variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring CRBAP under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding CRBAP or its derivatives possessing a substantially different codon usage, e.g., inclusion of non-
10 naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding CRBAP and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more desirable properties, such as a
15 greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode CRBAP and CRBAP derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell systems using reagents well known in the art. Moreover, synthetic chemistry may be used to
20 introduce mutations into a sequence encoding CRBAP or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:8-14, or fragments thereof, under various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.*
25 152:507-511.) For example, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and most preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, while high stringency hybridization can be obtained in the presence of at least about 35% formamide, and
30 most preferably at least about 50% formamide. Stringent temperature conditions will ordinarily include temperatures of at least about 30°C, more preferably of at least about 37°C, and most preferably of at least about 42°C. Varying additional parameters, such as hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS), and the inclusion or exclusion of carrier DNA, are well known to those skilled in the art. Various levels of stringency are

accomplished by combining these various conditions as needed. In a preferred embodiment, hybridization will occur at 30°C in 750 mM NaCl, 75 mM trisodium citrate, and 1% SDS. In a more preferred embodiment, hybridization will occur at 37°C in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 µg/ml denatured salmon sperm DNA (ssDNA). In a most preferred embodiment, hybridization will occur at 42°C in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50 % formamide, and 200 µg/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

The washing steps which follow hybridization can also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include temperature of at least about 25°C, more preferably of at least about 42°C, and most preferably of at least about 68°C. In a preferred embodiment, wash steps will occur at 25°C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a most preferred embodiment, wash steps will occur at 68°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art.

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Perkin-Elmer), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the Robbins Hydra microdispenser (Robbins Scientific, Sunnyvale CA), Hamilton MICROLAB 2200 (Hamilton, Reno NV), Peltier Thermal Cycler 200 (PTC200; MJ Research, Watertown MA) and the ABI CATALYST 800 (Perkin-Elmer). Sequencing is then carried out using the ABI 373 or 377 DNA sequencing systems (Perkin-Elmer), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding CRBAP may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR. Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3066.) Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 primer analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular, capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Perkin-Elmer), and the entire process from loading of samples to computer analysis and electronic data display may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments

which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode CRBAP may be cloned in recombinant DNA molecules that direct expression of CRBAP, or fragments or functional equivalents thereof, in appropriate host cells. Due to the
5 inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express CRBAP.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter CRBAP-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene
10 product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

In another embodiment, sequences encoding CRBAP may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) Nucl. Acids Res. Symp. Ser. 215-223, and Horn, T. et al. (1980) Nucl. Acids Res. Symp. Ser. 225-232.)
15 Alternatively, CRBAP itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solid-phase techniques. (See, e.g., Roberge, J.Y. et al. (1995) Science 269:202-204.) Automated synthesis may be achieved using the
20 ABI 431A peptide synthesizer (Perkin-Elmer). Additionally, the amino acid sequence of CRBAP, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

The peptide may be substantially purified by preparative high performance liquid
25 chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) Methods Enzymol. 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY.)

In order to express a biologically active CRBAP, the nucleotide sequences encoding CRBAP
30 or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding CRBAP. Such elements may vary in their strength and

specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding CRBAP. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding CRBAP and its initiation codon and upstream regulatory sequences are inserted into the appropriate expression vector, no
5 additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the
10 particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding CRBAP and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques,
15 synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons, New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express
20 sequences encoding CRBAP. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or
25 pBR322 plasmids); or animal cell systems. The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected depending upon the use intended for polynucleotide sequences encoding CRBAP. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding CRBAP can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or
30 PSFORT1 plasmid (Life Technologies). Ligation of sequences encoding CRBAP into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster

(1989) J. Biol. Chem. 264:5503-5509.) When large quantities of CRBAP are needed, e.g. for the production of antibodies, vectors which direct high level expression of CRBAP may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of CRBAP. A number of vectors
5 containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast *Saccharomyces cerevisiae* or *Pichia pastoris*. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, *supra*; Grant et al. (1987) Methods Enzymol. 153:516-54; and Scorer, C. A. et al. (1994)
10 Bio/Technology 12:181-184.)

Plant systems may also be used for expression of CRBAP. Transcription of sequences encoding CRBAP may be driven by viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) EMBO J. 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock
15 promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; and Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., *The McGraw Hill Yearbook of Science and Technology* (1992) McGraw Hill, New York NY, pp. 191-196.)

20 In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding CRBAP may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses CRBAP in host cells. (See, e.g., Logan, J. and T. Shenk
25 (1984) Proc. Natl. Acad. Sci. 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are
30 constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) Nat Genet. 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of CRBAP in cell lines is preferred. For example, sequences encoding CRBAP can be transformed

into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk* or *ap^r* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* or *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding CRBAP is inserted within a marker gene sequence, transformed cells containing sequences encoding CRBAP can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding CRBAP under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding CRBAP and that express CRBAP may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein

sequences.

Immunological methods for detecting and measuring the expression of CRBAP using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and
5 fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on CRBAP is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St Paul MN, Sect. IV; Coligan, J. E. et al. (1997) Current Protocols in Immunology, Greene Pub. Associates
10 and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding CRBAP
15 include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding CRBAP, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted
20 using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with nucleotide sequences encoding CRBAP may be cultured under
25 conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode CRBAP may be designed to contain signal sequences which direct secretion of CRBAP through a prokaryotic or eukaryotic cell membrane.

30 In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different

host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC, Bethesda MD) and may be chosen to ensure the correct modification and processing of the foreign protein.

5 In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding CRBAP may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric CRBAP protein containing a heterologous moiety that can be recognized by a commercially available antibody may facilitate the screening of peptide libraries for inhibitors of CRBAP activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the CRBAP encoding sequence and the heterologous protein sequence, so that CRBAP may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled CRBAP may be achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract systems (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, preferably ³⁵S-methionine.

Fragments of CRBAP may be produced not only by recombinant production, but also by direct peptide synthesis using solid-phase techniques. (See, e.g., Creighton, supra pp. 55-60.) Protein synthesis may be performed by manual techniques or by automation. Automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin-Elmer). Various fragments of CRBAP may be synthesized separately and then combined to produce the full length molecule.

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of CRBAP and human carbohydrate-associated proteins. In addition, the expression of CRBAP is closely associated with inflamed, gastrointestinal, infected, reproductive, neurological, proliferating, and cancerous tissues, tissues of the eye, and inflammation of the gut and secretory epithelium. Therefore, CRBAP appears to play a role in autoimmune/ inflammatory disorders, gastrointestinal disorders, infectious disorders, reproductive disorders, neurological disorders, eye disorders, and cell proliferative disorders, including cancer. In the treatment of neoplastic, autoimmune/inflammatory, gastrointestinal, and infectious disorders associated with increased CRBAP expression or activity, it is desirable to decrease the expression or activity of CRBAP. In the treatment of the above conditions associated with decreased CRBAP expression or activity, it is desirable to increase the expression or activity of CRBAP.

Therefore, in one embodiment, CRBAP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CRBAP. Examples of such disorders include, but are not limited to, an autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, X-linked agammaglobinemia of Bruton, common variable immunodeficiency (CVI), DiGeorge's syndrome (thymic hypoplasia), thymic dysplasia, isolated IgA deficiency, severe combined immunodeficiency disease (SCID), immunodeficiency with thrombocytopenia and eczema (Wiskott-Aldrich syndrome), Chediak-Higashi syndrome, chronic granulomatous diseases, hereditary angioneurotic edema, immunodeficiency associated with Cushing's disease, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a gastrointestinal disorder such as dysphagia, peptic esophagitis, esophageal spasm, esophageal stricture, esophageal carcinoma, dyspepsia, indigestion, gastritis, gastric carcinoma, anorexia, nausea, emesis,

gastroparesis, antral or pyloric edema, abdominal angina, pyrosis, gastroenteritis, intestinal obstruction, infections of the intestinal tract, peptic ulcer, cholelithiasis, cholecystitis, cholestasis, pancreatitis, pancreatic carcinoma, biliary tract disease, hepatitis, hyperbilirubinemia, cirrhosis, passive congestion of the liver, hepatoma, infectious colitis, ulcerative colitis, ulcerative proctitis,

5 Crohn's disease, Whipple's disease, Mallory-Weiss syndrome, colonic carcinoma, colonic obstruction, irritable bowel syndrome, short bowel syndrome, diarrhea, constipation, gastrointestinal hemorrhage, and acquired immunodeficiency syndrome (AIDS) enteropathy; an infectious disorder such as a viral infection, e.g., those caused by adenoviruses (acute respiratory disease, pneumonia),

10 arenaviruses (lymphocytic choriomeningitis), bunyaviruses (Hantavirus), coronaviruses (pneumonia, chronic bronchitis), hepadnaviruses (hepatitis), herpesviruses (herpes simplex virus, varicella-zoster virus, Epstein-Barr virus, cytomegalovirus), flaviviruses (yellow fever), orthomyxoviruses (influenza), papillomaviruses (cancer), paramyxoviruses (measles, mumps), picornoviruses (rhinovirus, poliovirus, coxsackie-virus), polyomaviruses (BK virus, JC virus), poxviruses (smallpox), reovirus (Colorado tick fever), retroviruses (human immunodeficiency virus, human T

15 lymphotropic virus), rhabdoviruses (rabies), rotaviruses (gastroenteritis), and togaviruses (encephalitis, rubella), infections by bacterial agents classified as pneumococcus, staphylococcus, streptococcus, bacillus, corynebacterium, clostridium, meningococcus, gonococcus, listeria, moraxella, kingella, haemophilus, legionella, bordetella, gram-negative enterobacterium including shigella, salmonella, and campylobacter, pseudomonas, vibrio, brucella, francisella, yersinia,

20 bartonella, norcardium, actinomyces, mycobacterium, spirochaetale, rickettsia, chlamydia, and mycoplasma, infections by fungal agents classified as aspergillus, blastomyces, dermatophytes, cryptococcus, coccidioides, malassezia, histoplasma, and other fungal agents causing various mycoses, and infections by parasites classified as plasmodium or malaria-causing, parasitic entamoeba, leishmania, trypanosoma, toxoplasma, pneumocystis carinii, intestinal protozoa such as

25 giardia, trichomonas, tissue nematodes such as trichinella, intestinal nematodes such as ascaris, lymphatic filarial nematodes, trematodes such as schistosoma, and cestodes such as tapeworm; a reproductive disorder such as disorders of prolactin production; infertility, including tubal disease, ovulatory defects, and endometriosis; disruptions of the estrous cycle, disruptions of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian

30 tumors, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; disruptions of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's

disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease; prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome; fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis; inherited, metabolic, endocrine, and toxic myopathies; myasthenia gravis, periodic paralysis; mental disorders including mood, anxiety, and schizophrenic disorders; akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's disorder; an eye disorder such as conjunctivitis, keratoconjunctivitis sicca, keratitis, episcleritis, iritis, posterior uveitis, glaucoma including POAG, amaurosis fugax, ischemic optic neuropathy, optic neuritis, Leber's hereditary optic neuropathy, toxic optic neuropathy, vitreous detachment, retinal detachment, cataract, macular degeneration, central serous chorioretinopathy, retinitis pigmentosa, melanoma of the choroid, retrobulbar tumor, and chiasmal tumor; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus.

In another embodiment, a vector capable of expressing CRBAP or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CRBAP including, but not limited to, those described above.

In a further embodiment, a pharmaceutical composition comprising a substantially purified CRBAP in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CRBAP including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of CRBAP may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of CRBAP including, but not limited to, those listed above.

In a further embodiment, an antagonist of CRBAP may be administered to a subject to treat
5 or prevent a disorder associated with increased expression or activity of CRBAP. Such disorders may include, but are not limited to, those autoimmune/ inflammatory disorders, gastrointestinal disorders, infectious disorders, reproductive disorders, neurological disorders, eye disorders, and cell proliferative disorders, including cancer, discussed above. In one aspect, an antibody which specifically binds CRBAP may be used directly as an antagonist or indirectly as a targeting or
10 delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express CRBAP.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding CRBAP may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of CRBAP including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary
15 sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic
20 efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of CRBAP may be produced using methods which are generally known in the art. In particular, purified CRBAP may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind CRBAP. Antibodies to CRBAP may also be generated using methods that are well known in the art. Such antibodies may include, but are
25 not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are especially preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with CRBAP or with any fragment or oligopeptide
30 thereof which has immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are

especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to CRBAP have an amino acid sequence consisting of at least about 5 amino acids, and, more preferably, of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or
5 fragments are identical to a portion of the amino acid sequence of the natural protein and contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of CRBAP amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to CRBAP may be prepared using any technique which provides for
10 the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-
hybridoma technique. (See, e.g., Kohler, G. et al. (1975) *Nature* 256:495-497; Kozbor, D. et al. (1985) *J. Immunol. Methods* 81:31-42; Cote, R.J. et al. (1983) *Proc. Natl. Acad. Sci.* 80:2026-2030; and Cole, S.P. et al. (1984) *Mol. Cell Biol.* 62:109-120.)

15 In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) *Proc. Natl. Acad. Sci.* 81:6851-6855; Neuberger, M.S. et al. (1984) *Nature* 312:604-608; and Takeda, S. et al. (1985) *Nature* 314:452-454.) Alternatively, techniques described for the production of single
20 chain antibodies may be adapted, using methods known in the art, to produce CRBAP-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton D.R. (1991) *Proc. Natl. Acad. Sci.* 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte
25 population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) *Proc. Natl. Acad. Sci.* 86: 3833-3837; Winter, G. et al. (1991) *Nature* 349:293-299.)

Antibody fragments which contain specific binding sites for CRBAP may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by pepsin
30 digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) *Science* 246:1275-1281.)

Various immunoassays may be used for screening to identify antibodies having the desired

specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between CRBAP and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies
5 reactive to two non-interfering CRBAP epitopes is preferred, but a competitive binding assay may also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for CRBAP. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of CRBAP-antibody complex
10 divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple CRBAP epitopes, represents the average affinity, or avidity, of the antibodies for CRBAP. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular CRBAP epitope, represents a true measure of affinity. High-affinity antibody
15 preparations with K_a ranging from about 10^9 to 10^{12} l/mole are preferred for use in immunoassays in which the CRBAP-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 l/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of CRBAP, preferably in active form, from the antibody (Catty, D. (1988) Antibodies, Volume I: A Practical
20 Approach, IRL Press, Washington DC; Liddell, J. E. and Cryer, A. (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml,
25 preferably 5-10 mg specific antibody/ml, is preferred for use in procedures requiring precipitation of CRBAP-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding CRBAP, or any
30 fragment or complement thereof, may be used for therapeutic purposes. In one aspect, the complement of the polynucleotide encoding CRBAP may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding CRBAP. Thus, complementary molecules or fragments may be used to modulate CRBAP activity, or to achieve regulation of gene function. Such

technology is now well known in the art, and sense or antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding CRBAP.

Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or
5 from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. Methods which are well known to those skilled in the art can be used to construct vectors to express nucleic acid sequences complementary to the polynucleotides encoding CRBAP. (See, e.g., Sambrook, supra; Ausubel, 1995, supra.)

Genes encoding CRBAP can be turned off by transforming a cell or tissue with expression
10 vectors which express high levels of a polynucleotide, or fragment thereof, encoding CRBAP. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector, and may last even longer if appropriate replication elements are part of
15 the vector system.

As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5', or regulatory regions of the gene encoding CRBAP. Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, are preferred. Similarly,
20 inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco NY, pp. 163-
25 177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For
30 example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding CRBAP.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences: GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides,

corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

5 Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding CRBAP. Such DNA sequences may be incorporated into
10 a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3'
15 ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous
20 endonucleases.

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers may be
25 achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nature Biotechnology 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

30 An additional embodiment of the invention relates to the administration of a pharmaceutical or sterile composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of CRBAP, antibodies to CRBAP, and mimetics, agonists, antagonists, or inhibitors of CRBAP. The compositions may be administered alone or in combination with at least one other agent, such as a

stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs, or hormones.

The pharmaceutical compositions utilized in this invention may be administered by any
5 number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate
10 processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA).

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral
15 administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combining active compounds with solid excipient and processing the resultant mixture of granules (optionally, after
20 grinding) to obtain tablets or dragee cores. Suitable auxiliaries can be added, if desired. Suitable excipients include carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, and sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums, including arabic and tragacanth; and proteins, such as gelatin and collagen. If desired, disintegrating
25 or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, and alginic acid or a salt thereof, such as sodium alginate.

Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures.
30 Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with fillers or binders, such as lactose or

starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

Pharmaceutical formulations suitable for parenteral administration may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils, such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate, triglycerides, or liposomes. Non-lipid polycationic amino polymers may also be used for delivery. Optionally, the suspension may also contain suitable stabilizers or agents to increase the solubility of the compounds and allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, and succinic acid. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1 mM to 50 mM histidine, 0.1% to 2% sucrose, and 2% to 7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to use.

After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of CRBAP, such labeling would include amount, frequency, and method of administration.

Pharmaceutical compositions suitable for use in the invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, e.g., of neoplastic cells or in animal models such as mice, rats, rabbits, dogs, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for

administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example CRBAP or fragments thereof, antibodies of CRBAP, and agonists, antagonists or inhibitors of CRBAP, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic effects is the therapeutic index, and it can be expressed as the LD_{50}/ED_{50} ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind CRBAP may be used for the diagnosis of disorders characterized by expression of CRBAP, or in assays to monitor patients being treated with CRBAP or agonists, antagonists, or inhibitors of CRBAP. Antibodies useful for diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for CRBAP include methods which utilize the antibody and a label to detect CRBAP in human body fluids or in extracts of cells or tissues. The antibodies may be used with or

without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known in the art and may be used.

A variety of protocols for measuring CRBAP, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of CRBAP expression. Normal or standard values for CRBAP expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody to CRBAP under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, preferably by photometric means. Quantities of CRBAP expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding CRBAP may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which expression of CRBAP may be correlated with disease. The diagnostic assay may be used to determine absence, presence, and excess expression of CRBAP, and to monitor regulation of CRBAP levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding CRBAP or closely related molecules may be used to identify nucleic acid sequences which encode CRBAP. The specificity of the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low), will determine whether the probe identifies only naturally occurring sequences encoding CRBAP, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and should preferably have at least 50% sequence identity to any of the CRBAP encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:8-14 or from genomic sequences including promoters, enhancers, and introns of the CRBAP gene.

Means for producing specific hybridization probes for DNAs encoding CRBAP include the cloning of polynucleotide sequences encoding CRBAP or CRBAP derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes *in vitro* by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a

variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

Polynucleotide sequences encoding CRBAP may be used for the diagnosis of disorders associated with expression of CRBAP. Examples of such disorders include, but are not limited to, an

- 5 autoimmune/inflammatory disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis,
- 10 diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome,
- 15 systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, X-linked agammaglobinemia of Bruton, common variable immunodeficiency (CVI), DiGeorge's syndrome (thymic hypoplasia), thymic dysplasia, isolated IgA deficiency, severe combined immunodeficiency disease (SCID), immunodeficiency with thrombocytopenia and eczema (Wiskott-Aldrich syndrome), Chediak-Higashi syndrome,
- 20 chronic granulomatous diseases, hereditary angioneurotic edema, immunodeficiency associated with Cushing's disease, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma; a gastrointestinal disorder such as dysphagia, peptic esophagitis, esophageal spasm, esophageal stricture, esophageal carcinoma, dyspepsia, indigestion, gastritis, gastric carcinoma, anorexia, nausea, emesis,
- 25 gastroparesis, antral or pyloric edema, abdominal angina, pyrosis, gastroenteritis, intestinal obstruction, infections of the intestinal tract, peptic ulcer, cholelithiasis, cholecystitis, cholestasis, pancreatitis, pancreatic carcinoma, biliary tract disease, hepatitis, hyperbilirubinemia, cirrhosis, passive congestion of the liver, hepatoma, infectious colitis, ulcerative colitis, ulcerative proctitis, Crohn's disease, Whipple's disease, Mallory-Weiss syndrome, colonic carcinoma, colonic
- 30 obstruction, irritable bowel syndrome, short bowel syndrome, diarrhea, constipation, gastrointestinal hemorrhage, and acquired immunodeficiency syndrome (AIDS) enteropathy; an infectious disorder such as a viral infection, e.g., those caused by adenoviruses (acute respiratory disease, pneumonia), arenaviruses (lymphocytic choriomeningitis), bunyaviruses (Hantavirus), coronaviruses (pneumonia, chronic bronchitis), hepadnaviruses (hepatitis), herpesviruses (herpes simplex virus, varicella-zoster

virus, Epstein-Barr virus, cytomegalovirus), flaviviruses (yellow fever), orthomyxoviruses (influenza), papillomaviruses (cancer), paramyxoviruses (measles, mumps), picornaviruses (rhinovirus, poliovirus, coxsackie-virus), polyomaviruses (BK virus, JC virus), poxviruses (smallpox), reovirus (Colorado tick fever), retroviruses (human immunodeficiency virus, human T lymphotropic virus), rhabdoviruses (rabies), rotaviruses (gastroenteritis), and togaviruses (encephalitis, rubella), infections by bacterial agents classified as pneumococcus, staphylococcus, streptococcus, bacillus, corynebacterium, clostridium, meningococcus, gonococcus, listeria, moraxella, kingella, haemophilus, legionella, bordetella, gram-negative enterobacterium including shigella, salmonella, and campylobacter, pseudomonas, vibrio, brucella, francisella, yersinia, bartonella, norcardium, actinomyces, mycobacterium, spirochaetale, rickettsia, chlamydia, and mycoplasma, infections by fungal agents classified as aspergillus, blastomyces, dermatophytes, cryptococcus, coccidioides, malassezia, histoplasma, and other fungal agents causing various mycoses, and infections by parasites classified as plasmodium or malaria-causing, parasitic entamoeba, leishmania, trypanosoma, toxoplasma, pneumocystis carinii, intestinal protozoa such as giardia, trichomonas, tissue nematodes such as trichinella, intestinal nematodes such as ascaris, lymphatic filarial nematodes, trematodes such as schistosoma, and cestodes such as tapeworm; a reproductive disorder such as disorders of prolactin production; infertility, including tubal disease, ovulatory defects, and endometriosis; disruptions of the estrous cycle, disruptions of the menstrual cycle, polycystic ovary syndrome, ovarian hyperstimulation syndrome, endometrial and ovarian tumors, uterine fibroids, autoimmune disorders, ectopic pregnancies, and teratogenesis; cancer of the breast, fibrocystic breast disease, and galactorrhea; disruptions of spermatogenesis, abnormal sperm physiology, cancer of the testis, cancer of the prostate, benign prostatic hyperplasia, prostatitis, Peyronie's disease, impotence, carcinoma of the male breast, and gynecomastia; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease; prion diseases including kuru, Creutzfeldt-Jakob disease, and Gerstmann-Straussler-Scheinker syndrome; fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorders of the central nervous system, cerebral palsy, neuroskeletal disorders, autonomic nervous system disorders, cranial

nerve disorders, spinal cord diseases, muscular dystrophy and other neuromuscular disorders, peripheral nervous system disorders, dermatomyositis and polymyositis; inherited, metabolic, endocrine, and toxic myopathies; myasthenia gravis, periodic paralysis; mental disorders including mood, anxiety, and schizophrenic disorders; akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's disorder; an eye disorder such as conjunctivitis, keratoconjunctivitis sicca, keratitis, episcleritis, iritis, posterior uveitis, glaucoma including POAG, amaurosis fugax, ischemic optic neuropathy, optic neuritis, Leber's hereditary optic neuropathy, toxic optic neuropathy, vitreous detachment, retinal detachment, cataract, macular degeneration, central serous chorioretinopathy, retinitis pigmentosa, melanoma of the choroid, retrobulbar tumor, and chiasmal tumor; and a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus. The polynucleotide sequences encoding CRBAP may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered CRBAP expression. Such qualitative or quantitative methods are well known in the art.

In a particular aspect, the nucleotide sequences encoding CRBAP may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding CRBAP may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding CRBAP in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

In order to provide a basis for the diagnosis of a disorder associated with expression of CRBAP, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a

sequence, or a fragment thereof, encoding CRBAP, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values
5 obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

Once the presence of a disorder is established and a treatment protocol is initiated, hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained
10 from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

With respect to cancer, the presence of an abnormal amount of transcript (either under- or over-expressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance
15 of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding CRBAP may involve the use of PCR. These oligomers may be chemically synthesized, generated
20 enzymatically, or produced *in vitro*. Oligomers will preferably contain a fragment of a polynucleotide encoding CRBAP, or a fragment of a polynucleotide complementary to the polynucleotide encoding CRBAP, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantitation of closely related DNA or RNA sequences.

25 Methods which may also be used to quantitate the expression of CRBAP include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) J. Immunol. Methods 159:235-244; Duplaa, C. et al. (1993) Anal. Biochem. 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in an ELISA format where the oligomer of
30 interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as targets in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously and to identify

genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, and to develop and monitor the activities of therapeutic agents.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) Proc. Natl. Acad. Sci. 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) Proc. Natl. Acad. Sci. 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

In another embodiment of the invention, nucleic acid sequences encoding CRBAP may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J. (1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) site. Correlation between the location of the gene encoding CRBAP on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The nucleotide sequences of the invention may be used to detect differences in gene sequences among normal, carrier, and affected individuals.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms by physical mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or syndrome has been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion,

etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, CRBAP, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between CRBAP and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with CRBAP, or fragments thereof, and washed. Bound CRBAP is then detected by methods well known in the art. Purified CRBAP can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding CRBAP specifically compete with a test compound for binding CRBAP. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with CRBAP.

In additional embodiments, the nucleotide sequences which encode CRBAP may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. [Attorney Docket No: PF-0604 P, filed October 1, 1998], U.S. Ser. No. [Attorney Docket No: PF-0605 P, filed October 6, 1998], U.S. Ser. No. [Attorney Docket No: PF-0639 P, filed November 13, 1998], and U.S. Ser. No. [Attorney Docket No: PF-0646 P, filed December 3, 1998] are hereby expressly incorporated by reference.

EXAMPLES

I. cDNA Library Construction

RNA was purchased from Clontech or isolated from tissues described in Table 4. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged
5 over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A⁺) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles
10 (QIAGEN, Valencia CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP
15 vector system (Stratagene) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, *supra*, units 5.1-6.6). Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-
20 1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSPORT1 plasmid (Life Technologies), or pINCY (Incyte Pharmaceuticals, Palo Alto CA). Recombinant plasmids were transformed into competent *E. coli*
25 cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids were recovered from host cells by cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an
30 AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a

high-throughput format (Rao, V.B. (1994) Anal. Biochem. 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a Fluoroskan II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

The cDNAs were prepared for sequencing using the ABI CATALYST 800 (Perkin-Elmer) or the HYDRA microdispenser (Robbins Scientific) or MICROLAB 2200 (Hamilton) systems in combination with the PTC-200 thermal cyclers (MJ Research). The cDNAs were sequenced using at least one of the following: the ABI PRISM 373 or 377 sequencing systems (Perkin-Elmer) and standard ABI protocols, base calling software, and kits; the MEGABACE 1000 DNA sequencing system (Molecular Dynamics); the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer); solutions and dyes from Amersham Pharmacia Biotech; or other methods known in the art. Reading frames for the ESTs were determined using standard methods (reviewed in Ausubel, 1997, supra, unit 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example V.

The polynucleotide sequences derived from cDNA and extension sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the tools, programs, and algorithms used and provides applicable descriptions, references, and threshold parameters. The first column of Table 5 shows the tools, programs, and algorithms used, the second column provides brief descriptions, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences). Sequences were analyzed using MACDNASIS PRO software (Hitachi Software Engineering) and LASERGENE software (DNASTAR).

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The sequences were then queried against a selection of public databases, such as GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS to acquire annotation, using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and were screened for open reading

frames using programs based on GeneMark, BLAST, and FASTA. The full length polynucleotide sequences were translated to derive the corresponding full length amino acid sequences, and these full length sequences were subsequently analyzed by querying against databases such as the GenBank databases, SwissProt, BLOCKS, PRINTS, Prosite, and Hidden Markov Model (HMM)-based protein family databases such as PFAM. HMM is a probabilistic approach which analyzes consensus primary structures of gene families. (See, e.g., Eddy, S.R. (1996) *Cur. Opin. Str. Biol.* 6:361-365.) Single nucleotide polymorphisms were discovered using Consed software (Gordon, D. et al. (1998) *Genome Research* 8:195-202; Nickerson, D.A. et al. (1997) *Nucleic Acids Research* 25:2745-2751).

- 10 The programs described above for the assembly and analysis of full length polynucleotide and amino acid sequences were used to identify polynucleotide sequence fragments from SEQ ID NO:8-14. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in The Invention section above.

IV. Northern Analysis

- 15 Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, *supra*, ch. 7; Ausubel, 1995, *supra*, ch. 4 and 16.)

- 20 Analogous computer techniques applying BLAST were used to search for identical or related molecules in nucleotide databases such as GenBank or LIFESEQ database (Incyte Pharmaceuticals, Palo Alto CA). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$25 \quad \frac{\% \text{ sequence identity} \times \% \text{ maximum BLAST score}}{100}$$

- The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1% to 2% error, and, with a product score of 70, the match will be exact. Similar molecules
30 are usually identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding CRBAP occurred. Analysis involved the categorization of cDNA libraries by organ/tissue and disease. The organ/tissue categories included cardiovascular,

dermatologic, developmental, endocrine, gastrointestinal, hematopoietic/immune, musculoskeletal, nervous, reproductive, and urologic. The disease/condition categories included cancer, inflammation/trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific expression are reported in Table 3.

V. Extension of CRBAP Encoding Polynucleotides

The full length nucleic acid sequence of SEQ ID NO:8-14 were produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer, to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and β -mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 μ l PICO GREEN quantitation reagent (0.25% (v/v) PICO GREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 μ l of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 μ l to 10 μ l aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions were successful in extending

the sequence.

The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For
5 shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with *Pfu* DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on
10 antibiotic-containing media, individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and *Pfu* DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min;
15 Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulphoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI
20 PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer).

In like manner, the nucleotide sequence of SEQ ID NO:8-14 is used to obtain 5' regulatory sequences using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

VI. Labeling and Use of Individual Hybridization Probes

25 Hybridization probes derived from SEQ ID NO:8-14 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 µCi of
30 [³²P]-adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech). An aliquot containing 10⁷ counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases:

Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature
5 under increasingly stringent conditions up to 0.1x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are analyzed and compared using autoradiography.

VII. Microarrays

A chemical coupling procedure and an ink jet device can be used to synthesize array elements on the surface of a substrate. (See, e.g., Baldeschweiler, *supra*.) An array analogous to a
10 dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced by hand or using available methods and machines and contain any appropriate number of elements. After hybridization, nonhybridized probes are removed and a scanner used to determine the levels and patterns of fluorescence. The degree of complementarity and the relative abundance of each
15 probe which hybridizes to an element on the microarray may be assessed through analysis of the scanned images.

Full-length cDNAs, Expressed Sequence Tags (ESTs), or fragments thereof may comprise the elements of the microarray. Fragments suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). Full-length cDNAs, ESTs, or
20 fragments thereof corresponding to one of the nucleotide sequences of the present invention, or selected at random from a cDNA library relevant to the present invention, are arranged on an appropriate substrate, e.g., a glass slide. The cDNA is fixed to the slide using, e.g., UV cross-linking followed by thermal and chemical treatments and subsequent drying. (See, e.g., Schena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645.) Fluorescent probes
25 are prepared and used for hybridization to the elements on the substrate. The substrate is analyzed by procedures described above.

VIII. Complementary Polynucleotides

Sequences complementary to the CRBAP-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring CRBAP. Although use of
30 oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of CRBAP. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a

complementary oligonucleotide is designed to prevent ribosomal binding to the CRBAP-encoding transcript.

IX. Expression of CRBAP

Expression and purification of CRBAP are achieved using bacterial or virus-based

- 5 expression systems. For expression of CRBAP in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac (tac)* hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g.,
- 10 BL21(DE3). Antibiotic resistant bacteria express CRBAP upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of CRBAP in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding CRBAP by either homologous recombination or bacterial-mediated
- 15 transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See Engelhard, E. K. et al. (1994) Proc. Natl. Acad. Sci. USA 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther.
- 20 7:1937-1945.)

In most expression systems, CRBAP is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on

25 immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from CRBAP at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on

30 metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch 10 and 16). Purified CRBAP obtained by these methods can be used directly in the following activity assay.

X. Demonstration of CRBAP Activity

CRBAP-1

CRBAP-1 activity is demonstrated as the ability to bind to β -galactoside sugars. CRBAP-1 is applied to a lactosyl-Sepharose column, and the column is eluted with 0.1 M lactose. The presence of CRBAP-1 in the eluate is detected by sodium dodecyl sulfate polyacrylamide gel electrophoresis and indicates the ability of CRBAP-1 to bind β -galactoside sugars.

5 CRBAP-2

CRBAP-2 activity is demonstrated as the ability to hydrolyze HA (Lepperdinger, supra). Radioactively labeled HA is immobilized on microtiter plates with the aid of 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide and N-hydroxy-sulfosuccinimide. The radioactivity solubilized after incubation with CRBAP-2 is measured using a liquid scintillation counter and is proportional to
10 the CRBAP-2 in the starting sample.

CRBAP-3

CRBAP-3 activity is associated with its ability to recognize, bind, and transport N-acetylglucosamine-bearing proteins. Therefore, CRBAP-3 activity is measured as the level of binding of N-acetylglucosamine-bearing peptides using affinity chromatography. CRBAP-3 is
15 attached to a solid phase (e.g. agarose) and ^{125}I -N3-labelled N-acetylglucosamine-containing peptide (e.g. bovine serum albumin; GlcNAc-BSA) is loaded onto the column and allowed to interact for 1 hour. The column is then washed with loading buffer and bound peptide is eluted by addition of buffer containing 0.5 M unlabelled N-acetylglucosamine. Fractions are collected and measured for radioactivity using a gamma counter. CRBAP-3 activity is directly proportional to the quantity of
20 bound radioactive peptide.

CRBAP-4 and CRBAP-5

An assay for CRBAP-4 or CRBAP-5 is based on the biochemical properties of olfactomedin (Snyder, supra). Post-translational glycosylation results in the attachment of carbohydrate moieties to olfactomedin. Glycosylated olfactomedin monomers bind with high
25 affinity to the lectin Ricinus communis agglutinin I (RCA), a plant protein that binds to carbohydrate, whereas other glycoproteins do not bind to RCA, suggesting that the carbohydrate composition of olfactomedin is unique. Therefore, the activity of CRBAP-4 or CRBAP-5 is demonstrated by its high-affinity binding to RCA. CRBAP-4 or CRBAP-5 is monomerized by treatment with reducing agent and further solubilized with CHAPS detergent. RCA conjugated to an
30 inert resin is added to this solution. After an appropriate incubation period, the mixture is centrifuged to separate the RCA-resin and any material bound to it from the unbound fraction. The RCA-resin is washed with reducing agent in the presence of detergent. Material bound with high affinity is specifically eluted from the RCA-resin with D-galactose, a sugar that competes for RCA carbohydrate binding sites. The amount of CRBAP-4 or CRBAP-5 in the unbound fraction and the

eluent is analyzed by SDS-polyacrylamide gel electrophoresis and western blot utilizing specific antibody directed against CRBAP-4 or CRBAP-5. The ratio of CRBAP-4 or CRBAP-5 in the eluent to that in the unbound fraction is proportional to the amount of CRBAP-4 or CRBAP-5 bound to RCA and is a direct measure of CRBAP-4 or CRBAP-5 activity.

5 CRBAP-6 and CRBAP-7

CRBAP-6 or CRBAP-7 is measured by the ability of C-type lectin to bind carbohydrates. Carbohydrates may be demonstrated by examining the ability of recombinant CRBAP-6 or CRBAP-7 to bind to affinity columns comprising carbohydrates (e.g., lactose, maltose, D-mannose, D-galactose, which are available from Sigma Chemical Corp., St. Louis MO) or by using the assay
10 described by Christa et al. (1994, FEBS Lett. 337:114-118). Preferably a soluble form of CRBAP-6 or CRBAP-7 (i.e., lacking the transmembrane domain) is expressed and applied to the affinity column.

Some C-type lectins are also known to agglutinate bacteria. The ability of CRBAP-6 or CRBAP-7 to agglutinate bacteria is examined using the assay described by Iovanna et al. (1991, J.
15 Biol. Chem. 266:24664-24669). Briefly, bacteria (e.g., *E. coli* strains KH802 or JM101) are grown at 37°C to stationary phase in Luria-Bertani (LB) medium. The bacteria are then collected by centrifugation and washed in phosphate-buffered saline (PBS). The washed bacteria are resuspended in PBS containing 0.5 mM CaCl₂ (PBS/CaCl₂) and are placed in the wells of microtiter plates at a concentration of approximately 5 x 10⁷ bacteria/200 µl PBS/CaCl₂. CRBAP-6 or CRBAP-7
20 (preferably in a soluble form) is then added at a variety of concentrations (e.g., 1 to 50 µg/ml) and the presence of macroscopic aggregation is monitored following a 3 hour incubation at 25°C. Concanavalin A and albumin at 50 µg/ml may be employed as positive and negative controls, respectively.

In another alternative, an assay for CRBAP-6 or CRBAP-7 activity measures the amount of
25 cell aggregation induced by overexpression of CRBAP-6 or CRBAP-7. In this assay, cultured cells such as NIH 3T3 are transfected with cDNA encoding CRBAP-6 or CRBAP-7 contained within a suitable mammalian expression vector under control of a strong promoter. Cotransfection with cDNA encoding a fluorescent marker protein, such as Green Fluorescent Protein (Clontech), is useful for identifying stable transfectants. The amount of cell agglutination, or clumping, associated
30 with transfected cells is compared with that associated with nontransfected cells. The amount of cell agglutination is proportional to CRBAP-6 or CRBAP-7 activity.

XI. Functional Assays

CRBAP function is assessed by expressing the sequences encoding CRBAP at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a

mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 µg of recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2 µg of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP, and to evaluate cellular properties, for example, their apoptotic state. FCM detects and quantifies the uptake of fluorescent molecules that diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of CRBAP on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding CRBAP and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding CRBAP and other genes of interest can be analyzed by northern analysis or microarray techniques.

XII. Production of CRBAP Specific Antibodies

CRBAP substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the CRBAP amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for

selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, ch. 11.)

Typically, oligopeptides 15 residues in length are synthesized using an ABI 431A Peptide Synthesizer (Perkin-Elmer) using fmoc-chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, supra.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

10 **XIII. Purification of Naturally Occurring CRBAP Using Specific Antibodies**

Naturally occurring or recombinant CRBAP is substantially purified by immunoaffinity chromatography using antibodies specific for CRBAP. An immunoaffinity column is constructed by covalently coupling anti-CRBAP antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is
15 blocked and washed according to the manufacturer's instructions.

Media containing CRBAP are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of CRBAP (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/CRBAP binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and CRBAP is collected.

20 **XIV. Identification of Molecules Which Interact with CRBAP**

CRBAP, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter reagent. (See, e.g., Bolton et al. (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled CRBAP, washed, and any
25 wells with labeled CRBAP complex are assayed. Data obtained using different concentrations of CRBAP are used to calculate values for the number, affinity, and association of CRBAP with the candidate molecules.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the
30 invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

PF-0604 PCT

TABLE 1

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	8	714029	PROSTUT01	620990F1 (PGANNOT01), 714029H1, 714029X315F1, and 714029X328F1 (PROSTUT01), 1338783F1 (COLNUT03), 1354746T6 (LUNGNOT09), 1376593F1 and 1376593T1 (LUNGNOT10), 2591130F6 (LUNGNOT22), 3427924T6 (BRSTNOR01), 3720846H1 (PENCNOT10), 4554976H1 (KERAUNTO1), and SZAH02052F1
2	9	1450775	PENITUT01	1450775H1 (PENITUT01), 2197778F6 (SPLNFET02), 2216628H1 (SINTFET03), 2240704F6 (PANCTUT02), 2745765H1 (LUNGUT01), 2830219F6 and 2830219H1 (TLYMNOT03), 2957078H1 (KIDNFET01), 3001459H1 (TLYMNOT06), and 3319368F6 (PROSBPT03)
3	10	3369350	CONNTUT04	1569729 (UTRSNOT05), 840896R1 (PROSTUT05), 3369350H1 (CONNTUT04), 1545419T1 (PROSTUT04), 864526R1 (BRAITUT03)
4	11	1648214	PROSTUT09	1648214H1 and 1648214X14 (PROSTUT09), 1258421F1 (MENITUT03), SAGA01200F1, SAGA02759F1, SBAA03843F2, SBAA01253F1, SAGA00437R1, SAGA02098F1
5	12	2743295	BRSTTUT14	2743295H1 and 2743295X310F1 (BRSTTUT14), 3109944H1 (BRSTTUT15), 1748824F6 (STOMTUT02), 4718554H1 (BRAIHCT02), 3820353H1 (BONSTUT01), 2598657F6 (UTRSNOT10), 960034R6 (BRSTTUT03), 1672040F6 (BLADNOT05)
6	13	2821011	ADRETUT06	2821011H1 and 2821011F6 (ADRETUT06), 4630324H1 (GBLADIT02), 2595195F6 and 2595945F6 (OVRTUT01), 988057T6 and 988057R6 (LVENNOT03)
7	14	2921920	SININOT04	2921920H1, 2921920F6, and 2921920T6 (SININOT04)

PF-0604 PCT

TABLE 2

Protein SEQ ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence	Identification	Analytical Methods
1	171	S4 T72 S155 T92 T159	N20	Vertebrate Galactoside-binding lectin: G58 - D165	Galectin - 8 (g2810994) [Homo sapiens]	PFAM, BLAST, Motifs
2	666	T9 S112 T236 S263 T346 S364 S410 T452 T501 S505 S515 T533 T554 T153 S398 S601	N227 N424 N588 N633	Signal Peptide: M1 - G56	Hyaluronidase (g144861) [Clostridium perfringens]	BLAST, SPScan, Motifs
3	307	S80 T194 S240 S210 T271		Signal Peptide: M1 - R37	TGR-CL10C (g1247124) [Homo sapiens]	BLAST, HMM, SPScan, Motifs
4	402	T118 T185 T232 T245 T268 T295 T350 S352 S150 S172 T390 T395 Y101 Y104	N66 N138 N183	Signal Peptide: M1 - A26 Potential glycosaminoglycan attachment site: S284 - G287 C-terminal region of extracellular proteins: G335 - P357	Neuronal olfactomedin- related ER localized protein (g442368) [Rattus norvegicus]	BLAST, BLOCKS,, HMM, SPScan, Motifs
5	409	S38 S97 S139 T197 S277 T317 T381 S97 T115 S215 T322 Y377	N354		Neuronal olfactomedin- related ER localized protein (g442368) [Rattus norvegicus]	BLAST, Motifs
6	271	S90 Y154		Signal Peptide: M1 - L20 Collagen-like domain: G41 - P112 C-type lectin domain: A247 - C256 C1q domain protein sequence: G44 - G77 C-type lectin family sequence: E150 - E265	Lung surfactant protein D (g415939) [Bos taurus]	BLAST, HMM, SPScan, BLOCKS, ProfileScan, PFAM
7	325	S30 S52 S62 T80 S96 T107 T142 S296 S52 S208		Signal Peptide: M1 - A26 Potential glycosaminoglycan attachment site: S86 - G89	Intelectin (g3357909) [Mus musculus]	BLAST, HMM, SPScan, Motifs

PF-0604 PCT

TABLE 3

SEQ ID NO:	Useful Fragment	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
8	465 - 500	Reproductive (0.327) Nervous (0.163) Gastrointestinal (0.122) Developmental (0.102)	Cell Proliferation (0.673) Inflammation (0.204)	PBLUESCRIPT
9	162 - 191	Reproductive (0.197) Hematopoietic/Immune (0.180) Cardiovascular (0.164) Nervous (0.148) Developmental (0.115)	Cell Proliferation (0.541) Inflammation (0.361)	pINCY
10	286 - 345	Reproductive (0.253) Nervous (0.200) Gastrointestinal (0.179)	Cancer (0.540) Inflammation (0.232)	pINCY
11	649 - 693	Reproductive (0.400) Gastrointestinal (0.160) Developmental (0.120) Nervous (0.120)	Cancer (0.800)	pINCY
12	334 - 378	Reproductive (0.480) Gastrointestinal (0.210)	Cancer (0.550) Inflammation (0.240)	pINCY
13	168 - 218	Gastrointestinal (0.368) Reproductive (0.158) Urologic (0.105) Cardiovascular (0.105) Developmental (0.105) Endocrine (0.105)	Cancer (0.368) Inflammation/trauma (0.315) Cell Proliferation (0.263)	pINCY
14	129 - 200	Gastrointestinal (0.556) Reproductive (0.222) Cardiovascular (0.222)	Cancer (0.556) Inflammation (0.444)	pINCY

PF-0604 PCT

TABLE 4

Nucleotide SEQ ID NO:	Clone ID	Library	Library Description
8	714029	PROSTUT01	Library was constructed using RNA isolated from the prostate tumor tissue removed from a 50-year-old Caucasian male. Pathology indicated grade 3 adenocarcinoma (Gleason grade 3+3). Patient history included dysuria, carcinoma in situ of prostate, coronary atherosclerosis, and hyperlipidemia.
9	1450775	PENITUT01	Library was constructed using RNA isolated from tumor tissue removed from the penis of a 64-year-old Caucasian male during penile amputation. Pathology indicated a fungating invasive grade 4 squamous cell carcinoma involving the inner wall of the foreskin and extending onto the glans penis. Patient history included benign neoplasm of the large bowel, atherosclerotic coronary artery disease, angina pectoris, gout, and obesity. Family history included malignant pharyngeal neoplasm, chronic lymphocytic leukemia, and chronic liver disease.
10	3369350	CONNTUT04	The library was constructed using RNA isolated from tumorous spinal soft tissue removed from a 35-year-old Caucasian male during an exploratory laparotomy. Pathology indicated schwannoma with degenerative changes. Patient history included anxiety, depression, benign hypertension, neurofibromatosis, and benign neoplasm of the scrotum. Family history included brain cancer, liver disease, and multiple sclerosis.
11	1648214	PROSTUT09	The library was constructed using RNA isolated from prostate tumor tissue removed from a 66-year-old Caucasian male during a radical prostatectomy, radical cystectomy, and urinary diversion. Pathology indicated grade 3 transitional cell carcinoma. Patient history included lung neoplasm, benign hypertension, and tobacco abuse in remission. Family history included malignant breast neoplasm, tuberculosis, benign hypertension, cerebrovascular disease, atherosclerotic coronary artery disease, and lung cancer.
12	2743295	BRSTTUT14	The library was constructed using RNA isolated from breast tumor tissue removed from a 62-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated an invasive grade 3 (of 4), nuclear grade 3 (of 3) adenocarcinoma, ductal type, located in the upper outer quadrant. Metastatic adenocarcinoma was identified in one (of 14) axillary lymph nodes. Immunohistochemical stains showed the tumor cells were strongly positive for estrogen receptors and weakly positive for progesterone receptors. Patient history included a benign colon neoplasm, hyperlipidemia, cardiac dysrhythmia, and obesity. Family history included atherosclerotic coronary artery disease, myocardial infarction, colon cancer, ovary cancer, lung cancer, and cerebrovascular disease.
13	2821011	ADRETUT06	The library was constructed using RNA isolated from adrenal tumor tissue removed from a 57-year-old Caucasian female during a unilateral right adrenalectomy. Pathology indicated pheochromocytoma (chromaffin cell tumor), forming a nodular mass completely replacing the medulla of the adrenal gland.
14	2921920	SININOT04	The library was constructed using RNA isolated from diseased ileum tissue removed from a 26-year-old Caucasian male during a partial colectomy, permanent colostomy, and an incidental appendectomy. Pathology indicated moderately to severely active Crohn's disease. Family history included regional enteritis of the small intestine.

Table 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25: 3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183: 63-98; and Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLOCKS IMPROVED Searcher that matches a sequence against those in BLOCKS and PRINTS databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff, Nucl. Acid Res., 19:6565-72, 1991. J.G. Henikoff and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37: 417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and Probability value= 1.0E-3 or less
PFAM	A Hidden Markov Models-based application useful for protein family search.	Krogh, A. et al. (1994) J. Mol. Biol., 235:1501- 1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits, depending on individual protein families

Table 5 (continued)

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25: 217-221.	Score= 4.0 or greater
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M. S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12: 431-439.	Score=5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch et al. <i>supra</i> ; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. A substantially purified polypeptide comprising the amino acid sequence of SEQ ID NO:1 and SEQ ID NO:3-7, and fragments thereof.
- 5 2. A substantially purified variant having at least 90% amino acid sequence identity to the amino acid sequence of claim 1.
3. An isolated and purified polynucleotide encoding the polypeptide of claim 1 or a fragment thereof.
4. An isolated and purified polynucleotide variant having at least 70% polynucleotide
10 sequence identity to the polynucleotide of claim 3.
5. An isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide of claim 3.
6. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide of claim 3.
- 15 7. A method for detecting a polynucleotide, the method comprising the steps of:
 - (a) hybridizing the polynucleotide of claim 6 to at least one nucleic acid in a sample, thereby forming a hybridization complex; and
 - (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of the polynucleotide in the sample.
- 20 8. The method of claim 7 further comprising amplifying the polynucleotide prior to hybridization.
9. An isolated and purified polynucleotide comprising the polynucleotide sequence of SEQ ID NO:8-14, and fragments thereof.
10. An isolated and purified polynucleotide variant having at least 70% polynucleotide
25 sequence identity to the polynucleotide of claim 9.
11. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide of claim 9.
12. An expression vector comprising at least a fragment of the polynucleotide of claim 3.
13. A host cell comprising the expression vector of claim 12.
- 30 14. A method for producing a polypeptide, the method comprising the steps of:
 - (a) culturing the host cell of claim 13 under conditions suitable for the expression of the polypeptide; and
 - (b) recovering the polypeptide from the host cell culture.
15. A pharmaceutical composition comprising the polypeptide of claim 1 in conjunction

with a suitable pharmaceutical carrier.

16. A purified antibody which specifically binds to the polypeptide of claim 1.

17. A purified agonist of the polypeptide of claim 1.

18. A purified antagonist of the polypeptide of claim 1.

5 19. A method for treating or preventing a disorder associated with decreased expression or activity of CRBAP, the method comprising administering to a subject in need of such treatment an effective amount of the pharmaceutical composition of claim 15.

20. A method for treating or preventing a disorder associated with increased expression or activity of CRBAP, the method comprising administering to a subject in need of such treatment an
10 effective amount of the antagonist of claim 18.

21. The polynucleotide of claim 9 comprising the polynucleotide sequence of SEQ ID NO:8 which contains a single nucleotide polymorphism with C replacing T at position 428.

95	Q	L	L	R	N	S	C	I	S	G	E	R	G	E	E	Q	S	A	I	P	Y	F	F	F	I	P	D	Q	P	F	714029
237	A	F	V	R	N	S	F	L	Q	E	S	W	G	E	E	E	R	N	I	T	S	F	F	F	S	P	G	M	Y	F	GI 2810994
125	R	V	E	I	L	C	E	H	P	R	F	R	V	F	V	D	G	H	Q	L	F	D	F	Y	H	R	I	Q	T	L	714029
267	E	M	I	I	Y	C	D	V	R	E	F	K	V	A	V	N	G	V	H	S	L	E	Y	K	H	R	F	K	E	L	GI 2810994
155	S	A	I	D	T	I	K	I	N	G	D	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	714029
297	S	S	I	D	T	L	E	I	N	G	D	I	H	L	L	E	V	R	S	W											GI 2810994

FIGURE 1B

3/15

1	M	-	-	-	V	Q	K	E	S	Q	A	T	L	-	-	E	E	R	E	S	E	L	S	S	N	P	A	A	S	A	1450775
1	M	N	K	N	I	R	K	I	I	T	S	T	V	L	A	A	M	T	I	S	V	L	P	S	N	L	V	V	F	A	GI 144861
26	G	A	S	L	E	-	-	-	-	-	-	-	-	-	-	P	P	A	A	P	A	P	G	E	D	-	-	-	-	-	1450775
31	T	D	G	I	T	E	N	F	Y	E	I	Y	P	K	P	Q	E	I	S	Y	S	G	G	E	F	Q	I	S	D	E	GI 144861
41	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1450775	
61	I	N	I	V	Y	D	D	G	I	D	T	Y	T	K	K	R	V	D	E	V	L	E	A	S	N	L	E	A	T	V	GI 144861
50	V	A	G	A	A	G	A	R	R	F	L	C	G	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1450775
91	S	N	E	I	V	P	G	K	T	N	F	L	V	G	I	N	E	S	G	G	V	V	D	N	Y	F	N	K	N	I	GI 144861
65	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1450775	
121	P	H	D	E	S	F	F	D	E	K	M	D	A	N	I	V	S	V	K	D	G	V	I	G	V	I	A	E	D	T	GI 144861
65	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1450775	
151	D	S	A	F	Y	G	V	T	T	L	K	H	V	F	N	Q	L	E	E	G	N	E	I	K	N	F	R	A	D	D	GI 144861
65	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1450775	
181	Y	A	E	V	A	H	R	G	F	I	E	G	Y	Y	G	N	P	W	S	N	E	D	R	A	E	L	M	K	F	G	GI 144861
86	Q	K	W	E	L	N	T	Y	L	Y	A	P	K	D	D	Y	K	H	R	M	F	W	R	E	M	Y	S	V	E	E	1450775
211	G	D	Y	K	L	N	Q	Y	V	F	A	P	K	D	D	P	Y	H	N	S	K	W	R	D	L	Y	P	E	E	K	GI 144861

FIGURE 2A

4/15

116	A	E	Q	L	M	T	L	I	S	A	A	R	E	Y	E	I	E	F	I	Y	A	I	S	P	G	L	D	-	-	I	1450775		
241	L	S	E	I	K	K	L	A	Q	M	G	N	E	T	K	N	R	Y	V	Y	A	L	H	P	F	M	N	N	P	V	GI 144861		
144	T	F	S	N	-	-	-	P	K	E	V	S	T	L	K	R	K	L	D	Q	V	S	Q	F	G	C	R	S	F	1450775			
271	R	F	D	T	E	E	N	Y	Q	N	D	L	G	V	I	K	A	K	F	T	Q	L	L	E	N	D	V	R	Q	F	GI 144861		
170	A	L	L	F	D	D	I	D	H	N	M	C	A	A	D	K	E	V	F	S	S	F	A	H	A	Q	V	S	-	I	1450775		
301	A	I	L	A	D	D	A	S	A	P	-	-	A	Q	G	A	S	M	Y	V	K	L	L	T	D	L	T	R	W	L	GI 144861		
199	T	N	E	I	Y	Q	Y	L	G	E	P	E	T	F	L	F	C	P	T	E	Y	C	G	T	F	C	Y	P	N	V	1450775		
329	E	E	Q	Q	S	T	Y	P	D	L	K	T	D	L	M	F	C	P	S	D	Y	Y	G	N	-	-	-	-	-	GI 144861			
229	S	Q	S	P	Y	L	R	T	V	G	E	K	L	L	P	G	I	E	V	L	W	T	G	P	K	V	-	-	-	V	1450775		
353	G	S	S	A	Q	L	K	E	L	-	N	K	A	E	D	N	V	S	I	V	M	T	G	G	R	I	W	G	E	V	GI 144861		
256	S	K	E	I	P	V	E	S	I	E	E	V	S	K	I	I	K	-	-	R	A	P	V	I	W	D	N	I	H	A	1450775		
382	D	E	N	F	A	N	N	F	M	N	N	I	S	T	E	G	H	P	G	R	A	P	F	F	W	I	N	W	P	C	GI 144861		
284	N	D	Y	D	Q	K	R	L	F	L	G	P	Y	K	G	R	S	T	E	L	I	P	-	-	-	-	-	-	-	R	L	K	1450775
412	S	D	N	S	K	Q	H	L	I	M	G	-	-	-	G	N	D	T	F	L	H	P	G	V	D	P	S	K	I	D	GI 144861		
309	G	V	L	T	N	P	N	C	E	F	F	E	A	N	Y	V	A	I	H	T	L	A	-	-	-	-	-	-	-	-	-	1450775	
439	G	I	V	L	N	P	M	Q	Q	A	E	A	N	K	S	A	L	F	A	I	A	D	Y	A	W	N	I	W	D	N	GI 144861		

FIGURE 2B

5/15

332	- - - - -	Y K S N	- - - - -	- - - - -	M N	1450775
469	K E A D E N W N D S F K Y	M D H G T A E E T N S S L A L R	G I	144861		
338	G V R K D V V M T D S E	D S T V S I Q I K L E	-	1450775		
499	E I S K H M I N Q N M D G R V R P L Q E S V E L A P K L E A	A	G I	144861		
361	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	1450775
529	F K Q K Y D S G A S I K E D A L E L I E E F T N L Q K A A E	- - - - -	- - - - -	- - - - -	- - - - -	G I 144861
361	- - - - -	N E G S D E I E T D V L Y	S P Q M A	- - - - -	- - - - -	1450775
559	Y Y K N N P G N E R T R D Q I I Y	W L N C W E D T M D A A I	G I	144861		
380	L K L A L T	E W L Q	- - - - -	- - - - -	E F G V	1450775
589	G Y L K S A I A I E E G D D E A A W A N Y S E A Q S A F E K	G I	144861			
394	P H Q Y S S R Q V A H S G	A K A S V V D G T P L V A A P S	1450775			
619	S K T Y G F H Y V D H T E Y A E V G V Q H I V P F I K S M G	G I	144861			
423	L N A T T V V T T V	- - - - -	- - - - -	- - - - -	- - - - -	1450775
649	Q N L S V V I G S I V D P N R I I A T Y I S N R Q D A P T G	- - - - -	- - - - -	- - - - -	- - - - -	G I 144861
433	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	1450775
679	N P D N I F D N N A S T E L V Y Q E P I M S Q G A A L S G	- - - - -	- - - - -	- - - - -	- - - - -	G I 144861

FIGURE 2C

6/15

447	- - -	E P T T L T K E E E K K Q P D E E P M D -	M V V E K Q	1450775
709	K Y S N	P I T L N N V E F L M G A N S N P N D T	M Q K A K I	GI 144861
473	E E T D H K N D N Q I L S E I V E A K M A E E L K P M D T D		1450775	
739	Q Y T V D G R E W I D L E E G V E Y T M P G A I K V E N L D		GI 144861	
503	K E S I A E S K S P E M S M Q E D - -	C I S D I A P M Q T D	1450775	
769	L K V R G V R L I A T E A R E N T W L G V R D I N V N K K E		GI 144861	
531	E Q T N K E Q F V P G - - -	P N E K P L Y T A E P V T L E D	1450775	
799	D S N S G V E F N P S L I R S E S W Q V Y E G N E A N L L D		GI 144861	
558	- - - - -	- - - - -	L Q L - - -	1450775
829	G D D N T G V W Y K T L N G D T S L A G E F I G L D L G K E		GI 144861	
561	- - -	L A D L F Y L P Y E H G P K G A Q M L R E F Q - - - -	1450775	
859	I K L D G I R F V I G K N G G S S D K W N K F K L E Y S L		GI 144861	
584	- - -	W L R A N S S V V S V N C K G K D S - - - -	1450775	
889	D N E S W T T I K E Y D K T G A P A G K D V I E E S F E T P		GI 144861	
602	- - - - -	E K I E E W R S - - - -	1450775	
919	I S A K Y I R L T N M E N I N K W L T F S E F A I V S D E L		GI 144861	

FIGURE 2D

7/15

610	- - - - -	RAAKFE	- - - - -	EMCGLV	MGMFT	RLSN	1450775
949	ESAGN	KENVYT	NT	ELDL	SLAKED	VTKLIP	GI 144861
631	CANRT	ILYDMY	- - - - -	SYVWD	IKSI	- - - - -	1450775
979	IDDL	SLNHGEY	IGV	KLNR	IKDL	SLNIN	LEIS
							GI 144861
651	- - - - -	MSMVKSF	- - - - -	VQW	LAFAN		1450775
1009	NDTG	LKLQSS	MNG	VEW	TEIT	DKNT	LEDGRY
							GI 144861
666							1450775
1039	VRLF						GI 144861

FIGURE 2E

8/15

1	M	R	R	G	R	A	G	P	G	R	A	G	G	A	R	S	A	S	W	M	S	R	L	R	A	L	L	G	L	G		3369350	
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1247124		
31	L	L	V	A	G	S	R	L	P	R	I	K	S	Q	T	I	A	C	R	S	G	P	T	W	G	P	Q	R	L		3369350		
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1247124		
61	N	S	G	G	R	W	D	S	E	V	M	A	S	T	V	V	K	Y	L	S	Q	E	E	A	Q	A	V	D	Q	E		3369350	
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1247124		
91	L	F	N	E	Y	Q	F	S	V	D	Q	L	M	E	L	A	G	L	S	C	A	T	A	I	A	K	A	Y	P	P		3369350	
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	GI 1247124		
121	T	S	M	S	R	S	P	P	T	V	L	V	I	C	G	P	G	N	N	G	G	D	G	L	V	C	A	R	H	L		3369350	
1	-	-	-	-	-	-	-	-	-	G	P	T	V	L	V	I	C	G	P	G	N	N	G	G	D	G	L	V	C	A	R	H	GI 1247124
151	K	L	F	G	Y	E	P	T	I	Y	Y	P	K	R	P	N	K	P	L	F	T	A	L	V	T	Q	C	Q	K	M		3369350	
25	K	L	F	G	Y	E	P	T	I	Y	Y	P	K	R	P	N	K	P	L	F	T	A	L	V	T	Q	C	Q	K	M		GI 1247124	

FIGURE 3A

9/15

181	D I P F L G E M P A E P M T I D E L Y E L V V D A I F G F S	3369350
55	D I P F L G E M P A E P M T I D E L Y E L V V D A I F G F S	GI 1247124
211	F K G D V R E P F H S I L S V L K G L T V P I A S I D I P S	3369350
85	F K G D V R E P F H - - - - - - - - - - - - - - - - V P S	GI 1247124
241	G W D V E K G N A G G I Q P D L L I S L T A P K K S A T Q F	3369350
97		GI 1247124
271	T G R Y H Y L G G R F V P P A L E K K Y Q L N L P P Y P D T	3369350
97		GI 1247124
301	E C V Y R L Q	3369350
97		GI 1247124

FIGURE 3B

10/15

147	G	I	K	S	L	K	I	V	K	K	M	M	D	T	H	G	S	W	M	K	D	A	V	Y	N	S	P	-	-	K	1648214
159	T	I	T	G	P	T	T	Q	N	T	Y	G	R	N	E	G	A	W	M	K	D	P	L	A	K	-	-	D	E	R	2743295
204	G	I	S	D	P	V	T	V	K	T	S	G	S	R	F	G	S	W	M	T	D	P	L	A	P	E	G	D	N	R	GI 442368
175	V	Y	L	L	I	G	S	R	-	N	N	T	V	W	E	F	A	N	I	R	A	F	M	E	D	N	T	K	P	A	1648214
187	I	-	Y	V	T	N	Y	Y	G	N	T	L	V	E	F	R	N	L	E	N	F	K	Q	G	R	W	S	N	S	2743295	
234	V	W	Y	M	D	G	Y	H	N	N	R	F	V	R	E	Y	K	S	M	V	D	F	M	N	T	D	N	F	T	S	GI 442368
204	P	R	K	Q	I	L	T	L	S	W	Q	G	T	G	Q	V	I	Y	K	G	F	L	F	F	H	N	Q	A	T	S	1648214
216	Y	K	-	-	-	L	P	Y	S	W	I	G	T	G	H	V	V	Y	N	G	A	F	Y	Y	N	R	-	A	F	T	2743295
264	H	R	-	-	-	L	P	H	P	W	S	G	T	G	Q	V	V	Y	N	G	S	I	Y	F	N	K	-	F	Q	S	GI 442368
234	N	E	I	I	K	Y	N	L	Q	K	R	T	V	E	D	R	M	L	L	P	-	G	V	G	R	A	L	V	Y	1648214	
242	R	N	I	I	K	Y	D	L	K	Q	R	Y	V	A	A	W	A	M	L	H	D	V	A	Y	E	E	A	T	P	W	2743295
290	H	I	I	I	R	F	D	L	K	T	E	T	I	L	K	T	R	S	L	D	Y	A	G	Y	N	N	M	Y	H	Y	GI 442368
263	Q	H	S	P	S	T	Y	I	D	L	A	V	D	E	H	G	L	W	A	I	H	S	G	P	G	-	-	-	-	T	1648214
272	R	W	Q	G	H	S	D	V	D	F	A	V	D	E	N	G	L	W	L	I	Y	P	A	L	D	D	E	G	F	S	2743295
320	A	W	G	G	H	S	D	I	D	L	M	V	D	E	N	G	L	W	A	V	Y	A	T	N	Q	N	A	G	-	-	GI 442368

FIGURE 4A

11/15

289	H	S	H	L	V	L	T	K	I	E	P	G	T	L	G	V	E	-	-	H	S	W	D	P	C	R	S	Q	D	1648214		
302	Q	E	V	I	V	L	S	K	L	N	A	A	D	L	S	T	Q	K	E	T	T	W	R	T	G	L	R	R	N	F	2743295	
348	-	-	N	I	V	I	S	K	L	D	P	V	S	L	-	-	Q	I	L	Q	T	W	N	T	S	Y	P	K	R	S	GI 442368	
317	A	E	A	S	F	L	L	C	G	V	L	Y	V	V	Y	S	T	G	G	Q	G	P	H	R	I	T	C	I	Y	D	1648214	
332	Y	G	N	C	F	V	I	C	G	V	L	Y	A	V	D	S	Y	N	Q	R	N	A	-	N	I	S	Y	A	F	D	2743295	
374	A	G	E	A	F	I	I	C	G	T	L	Y	V	T	N	G	Y	S	G	-	G	T	-	K	V	H	Y	A	Y	Q	GI 442368	
347	P	L	G	T	I	S	E	E	D	L	P	N	L	F	F	P	K	R	P	R	S	H	S	M	I	H	Y	N	P	R	1648214	
361	-	-	-	T	H	T	N	T	Q	I	V	P	R	L	F	F	E	N	E	Y	S	T	T	Q	I	D	Y	N	P	K	2743295	
402	-	-	-	T	N	A	S	T	Y	E	I	D	I	P	F	F	Q	N	K	Y	S	H	I	S	M	L	D	Y	N	P	K	GI 442368
377	D	K	Q	L	Y	A	W	N	E	G	N	Q	I	T	Y	K	L	-	-	-	Q	T	K	R	K	L	P	L	K	1648214		
389	D	R	L	L	Y	A	W	D	N	G	H	Q	V	T	Y	H	V	I	F	-	-	-	-	-	-	-	-	A	Y	2743295		
430	D	R	A	L	Y	A	W	N	G	H	Q	T	L	Y	Y	N	V	T	L	F	H	V	I	R	S	D	E	L	GI 442368			

FIGURE 4B

12/15

```

1  MRGNLAL - VGVLLISLAFLLSL - - - - - 2821011
1  M - LLLPLS VLLLLLTQPPWRSLLGAEMK IY S Q K GI 415939

21  - - - - - 2821011
30  TMANACTLVMCSPPEEDGLPGRDGRDGREGP GI 415939

21  - - - - - 2821011
60  RGEKGDPSGPGPAGRAGMPGPAGPIGLKGD GI 415939

21  - - - - - 2821011
90  NGSAGEPPGPKGDTGPPGPPGMPGPAGREGP GI 415939

28  AGDDACSVQILVPGLLKGDAGEEKGDKGAPGR 2821011
120 SGKQGSMPGPPGTPGPKGDTGPKGVGAPGI GI 415939

58  PGRVGP TG EKGDMDKGQKGSVGRHGKI GP 2821011
150 QGSPGPAGLKG ERGAPGEPGAPGRAGAPGP GI 415939

88  IGSKEKGDSDIGPPGPNGEPLP - - - - - 2821011
180 AGAIGPPQPSGARGPPLKGDRTPGERGA GI 415939

```

FIGURE 5A

13/15

113	- - - - -	C E C S Q L R K A I G E M D N Q V S Q L T S E L	2821011
210	K G E S G L A E V N A L R Q R V G I L E G Q L Q R L Q N A F	GI 415939	
137	K F I K N A V - -	A G V R E T E S K I Y L L V K E E K R Y A	2821011
240	S Q Y K K A M L F P N G R S V G E K I F K T V G S E K T F Q	GI 415939	
165	D A Q L S C Q G R G G T L S M P K D E A A N G L M A Y L A	2821011	
270	D A Q Q I C T Q A G G Q L P S P R S G A E N E A L T Q - L A	GI 415939	
195	Q A G L A R V F I G I N D L E K E G A F V Y S D H S P M R T	2821011	
299	T A Q N K A A F L S M S D T R K E G T F I Y P T G E P L - V	GI 415939	
225	F N K W R S G E P N N A Y D E E D C V E M V A S G G W N D V	2821011	
328	Y S N W A P Q E P N N D G G S E N C V E I F P N G K W N D K	GI 415939	
255	A C H T T M Y F M C E F D K E N M	2821011	
358	V C G E Q R L V I C E F	GI 415939	

FIGURE 5B

1	M L S M L R T M T R L C F L L F F S V A T S G C S A A A S	2921920
1	M - - - - - T Q L G F L L F I M V A T R G C S A A E E N	GI 3357909
31	- S L E M L S R E F F E T C A F S F S S L P R S C K E I K E R	2921920
24	L D T N R W G N S F - - - - - F S S L P R S C K E I K Q E	GI 3357909
60	C H S A G D G L Y F L R T K N G V V Y Q T F C D M T S G G G	2921920
48	H T K A Q D G L Y F L R T K N G V I Y Q T F C D M T T A G G	GI 3357909
90	G W T L V A S V H E N D M H G K C T V G D R W S S Q Q G N K	2921920
78	G W T L V A S V H E N M R G K C T V G D R W S S Q Q G N R	GI 3357909
120	A D Y P E G D G N W A N Y N T F G S A E A A T S D D Y K N P	2921920
108	A D Y P E G D G N W A N Y N T F G S A E A A T S D D Y K N P	GI 3357909
150	G Y Y D I Q A K D L G I W H V P N K S P M Q H W R N S A L L	2921920
138	G Y F D I Q A E N L G I W H V P N K S P L H N W R K S S L L	GI 3357909
180	R Y R T N T G F L Q R L G H N L F G I Y Q K Y P V K Y R S G	2921920
168	R Y R T F T G F L Q H L G H N L F G L Y K K Y P V K Y G E G	GI 3357909

FIGURE 6A

15/15

210	K C W N D N G P A I P V V Y D F G D A K K T A S Y Y S P Y G	2921920
198	K C W T D N G P A L P V V Y D F G D A R K T A S Y Y S P S G	GI 3357909
240	Q R E F V A G F V Q F R V F N N E R A A N A L C A G I K V T	2921920
228	Q R E F T A G Y V Q F R V F N N E R A A S A L C A G V R V T	GI 3357909
270	G C N T E H H C I G G G G F F P Q G K P R Q C C G D F S A F D	2921920
258	G C N T E H H C I G G G G F F P E G N P V Q C C G D F A S F D	GI 3357909
300	W D G Y G T H V K S S C S R E I T E A A V L L F Y R	2921920
288	W D G Y G T H N G Y S S S R K I T E A A V L L F Y R	GI 3357909

FIGURE 6B

SEQUENCE LISTING

<110> INCYTE PHARMACEUTICALS, INC.
 AU-YOUNG, Janice
 LAL, Preeti
 BANDMAN, Olga
 REDDY, Roopa
 BAUGHN, Mariah R.
 YUE, Henry
 HILLMAN, Jennifer L.

<120> HUMAN CARBOHYDRATE-ASSOCIATED PROTEINS

<130> PF-0604 PCT

<140> To Be Assigned

<141> Herewith

<150> 09/164,785; unassigned; 09/167,179; unassigned; 09/191,838;
 unassigned; 09/205,656; unassigned

<151> 1998-10-01; 1998-10-01; 1998-10-06; 1998-10-06; 1998-11-13;
 1998-11-13; 1998-12-03; 1998-12-03

<160> 20

<170> FastSEQ 3.0

<210> 1

<211> 171

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID NO: 714029CD1

<400> 1

Met	Ala	Gly	Ser	Val	Ala	Asp	Ser	Asn	Ala	Val	Val	Lys	Leu	Asp
1				5					10					15
Asp	Gly	His	Leu	Asn	Asn	Ser	Leu	Ser	Ser	Pro	Val	Gln	Ala	Asp
			20						25					30
Val	Tyr	Phe	Pro	Arg	Leu	Ile	Val	Pro	Phe	Cys	Gly	His	Ile	Lys
			35						40					45
Gly	Gly	Met	Arg	Pro	Gly	Lys	Lys	Val	Leu	Val	Met	Gly	Ile	Val
			50						55					60
Asp	Leu	Asn	Pro	Glu	Ser	Phe	Ala	Ile	Ser	Leu	Thr	Cys	Gly	Asp
			65						70					75
Ser	Glu	Asp	Pro	Pro	Ala	Asp	Val	Ala	Ile	Glu	Leu	Lys	Ala	Val
			80						85					90
Phe	Thr	Asp	Arg	Gln	Leu	Leu	Arg	Asn	Ser	Cys	Ile	Ser	Gly	Glu
			95						100					105
Arg	Gly	Glu	Glu	Gln	Ser	Ala	Ile	Pro	Tyr	Phe	Pro	Phe	Ile	Pro
			110						115					120
Asp	Gln	Pro	Phe	Arg	Val	Glu	Ile	Leu	Cys	Glu	His	Pro	Arg	Phe
			125						130					135
Arg	Val	Phe	Val	Asp	Gly	His	Gln	Leu	Phe	Asp	Phe	Tyr	His	Arg

	140		145		150
Ile Gln Thr Leu	Ser Ala Ile Asp Thr	Ile Lys Ile Asn Gly	Asp		
	155		160		165
Leu Gln Ile Thr	Lys Leu				
	170				

<210> 2

<211> 666

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID NO: 1450775CD1

<400> 2

Met Val Gln Lys Glu Ser Gln Ala Thr Leu Glu Glu Arg Glu Ser		
1	5	10 15
Glu Leu Ser Ser Asn Pro Ala Ala Ser Ala Gly Ala Ser Leu Glu		
	20	25 30
Pro Pro Ala Ala Pro Ala Pro Gly Glu Asp Asn Pro Ala Gly Ala		
	35	40 45
Gly Gly Ala Ala Val Ala Gly Ala Ala Gly Gly Ala Arg Arg Phe		
	50	55 60
Leu Cys Gly Val Val Glu Gly Phe Tyr Gly Arg Pro Trp Val Met		
	65	70 75
Glu Gln Arg Lys Glu Leu Phe Arg Arg Leu Gln Lys Trp Glu Leu		
	80	85 90
Asn Thr Tyr Leu Tyr Ala Pro Lys Asp Asp Tyr Lys His Arg Met		
	95	100 105
Phe Trp Arg Glu Met Tyr Ser Val Glu Glu Ala Glu Gln Leu Met		
	110	115 120
Thr Leu Ile Ser Ala Ala Arg Glu Tyr Glu Ile Glu Phe Ile Tyr		
	125	130 135
Ala Ile Ser Pro Gly Leu Asp Ile Thr Phe Ser Asn Pro Lys Glu		
	140	145 150
Val Ser Thr Leu Lys Arg Lys Leu Asp Gln Val Ser Gln Phe Gly		
	155	160 165
Cys Arg Ser Phe Ala Leu Leu Phe Asp Asp Ile Asp His Asn Met		
	170	175 180
Cys Ala Ala Asp Lys Glu Val Phe Ser Ser Phe Ala His Ala Gln		
	185	190 195
Val Ser Ile Thr Asn Glu Ile Tyr Gln Tyr Leu Gly Glu Pro Glu		
	200	205 210
Thr Phe Leu Phe Cys Pro Thr Glu Tyr Cys Gly Thr Phe Cys Tyr		
	215	220 225
Pro Asn Val Ser Gln Ser Pro Tyr Leu Arg Thr Val Gly Glu Lys		
	230	235 240
Leu Leu Pro Gly Ile Glu Val Leu Trp Thr Gly Pro Lys Val Val		
	245	250 255
Ser Lys Glu Ile Pro Val Glu Ser Ile Glu Glu Val Ser Lys Ile		
	260	265 270
Ile Lys Arg Ala Pro Val Ile Trp Asp Asn Ile His Ala Asn Asp		
	275	280 285
Tyr Asp Gln Lys Arg Leu Phe Leu Gly Pro Tyr Lys Gly Arg Ser		
	290	295 300
Thr Glu Leu Ile Pro Arg Leu Lys Gly Val Leu Thr Asn Pro Asn		

	305	310	315
Cys Glu Phe Glu	Ala Asn Tyr Val Ala	Ile His Thr Leu Ala Thr	
	320	325	330
Trp Tyr Lys Ser	Asn Met Asn Gly Val	Arg Lys Asp Val Val Met	
	335	340	345
Thr Asp Ser Glu	Asp Ser Thr Val Ser	Ile Gln Ile Lys Leu Glu	
	350	355	360
Asn Glu Gly Ser	Asp Glu Asp Ile Glu	Thr Asp Val Leu Tyr Ser	
	365	370	375
Pro Gln Met Ala	Leu Lys Leu Ala Leu	Thr Glu Trp Leu Gln Glu	
	380	385	390
Phe Gly Val Pro	His Gln Tyr Ser Ser	Arg Gln Val Ala His Ser	
	395	400	405
Gly Ala Lys Ala	Ser Val Val Asp Gly	Thr Pro Leu Val Ala Ala	
	410	415	420
Pro Ser Leu Asn	Ala Thr Thr Val Val	Thr Thr Val Tyr Gln Glu	
	425	430	435
Pro Ile Met Ser	Gln Gly Ala Ala Leu	Ser Gly Glu Pro Thr Thr	
	440	445	450
Leu Thr Lys Glu	Glu Glu Lys Lys Gln	Pro Asp Glu Glu Pro Met	
	455	460	465
Asp Met Val Val	Glu Lys Gln Glu Glu	Thr Asp His Lys Asn Asp	
	470	475	480
Asn Gln Ile Leu	Ser Glu Ile Val Glu	Ala Lys Met Ala Glu Glu	
	485	490	495
Leu Lys Pro Met	Asp Thr Asp Lys Glu	Ser Ile Ala Glu Ser Lys	
	500	505	510
Ser Pro Glu Met	Ser Met Gln Glu Asp	Cys Ile Ser Asp Ile Ala	
	515	520	525
Pro Met Gln Thr	Asp Glu Gln Thr Asn	Lys Glu Gln Phe Val Pro	
	530	535	540
Gly Pro Asn Glu	Lys Pro Leu Tyr Thr	Ala Glu Pro Val Thr Leu	
	545	550	555
Glu Asp Leu Gln	Leu Leu Ala Asp Leu	Phe Tyr Leu Pro Tyr Glu	
	560	565	570
His Gly Pro Lys	Gly Ala Gln Met Leu	Arg Glu Phe Gln Trp Leu	
	575	580	585
Arg Ala Asn Ser	Ser Val Val Ser Val	Asn Cys Lys Gly Lys Asp	
	590	595	600
Ser Glu Lys Ile	Glu Glu Trp Arg Ser	Arg Ala Ala Lys Phe Glu	
	605	610	615
Glu Met Cys Gly	Leu Val Met Gly Met	Phe Thr Arg Leu Ser Asn	
	620	625	630
Cys Ala Asn Arg	Thr Ile Leu Tyr Asp	Met Tyr Ser Tyr Val Trp	
	635	640	645
Asp Ile Lys Ser	Ile Met Ser Met Val	Lys Ser Phe Val Gln Trp	
	650	655	660
Leu Ala Phe Ala	Ala Asn		
	665		

<210> 3

<211> 307

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID NO: 3369350CD1

<400> 3

```

Met Arg Arg Gly Arg Ala Gly Pro Gly Arg Ala Gly Gly Ala Arg
 1           5           10           15
Ser Ala Ser Trp Met Ser Arg Leu Arg Ala Leu Leu Gly Leu Gly
          20           25           30
Leu Leu Val Ala Gly Ser Arg Leu Pro Arg Ile Lys Ser Gln Thr
          35           40           45
Ile Ala Cys Arg Ser Gly Pro Thr Trp Trp Gly Pro Gln Arg Leu
          50           55           60
Asn Ser Gly Gly Arg Trp Asp Ser Glu Val Met Ala Ser Thr Val
          65           70           75
Val Lys Tyr Leu Ser Gln Glu Glu Ala Gln Ala Val Asp Gln Glu
          80           85           90
Leu Phe Asn Glu Tyr Gln Phe Ser Val Asp Gln Leu Met Glu Leu
          95          100          105
Ala Gly Leu Ser Cys Ala Thr Ala Ile Ala Lys Ala Tyr Pro Pro
          110          115          120
Thr Ser Met Ser Arg Ser Pro Pro Thr Val Leu Val Ile Cys Gly
          125          130          135
Pro Gly Asn Asn Gly Asp Gly Leu Val Cys Ala Arg His Leu
          140          145          150
Lys Leu Phe Gly Tyr Glu Pro Thr Ile Tyr Tyr Pro Lys Arg Pro
          155          160          165
Asn Lys Pro Leu Phe Thr Ala Leu Val Thr Gln Cys Gln Lys Met
          170          175          180
Asp Ile Pro Phe Leu Gly Glu Met Pro Ala Glu Pro Met Thr Ile
          185          190          195
Asp Glu Leu Tyr Glu Leu Val Val Asp Ala Ile Phe Gly Phe Ser
          200          205          210
Phe Lys Gly Asp Val Arg Glu Pro Phe His Ser Ile Leu Ser Val
          215          220          225
Leu Lys Gly Leu Thr Val Pro Ile Ala Ser Ile Asp Ile Pro Ser
          230          235          240
Gly Trp Asp Val Glu Lys Gly Asn Ala Gly Gly Ile Gln Pro Asp
          245          250          255
Leu Leu Ile Ser Leu Thr Ala Pro Lys Lys Ser Ala Thr Gln Phe
          260          265          270
Thr Gly Arg Tyr His Tyr Leu Gly Gly Arg Phe Val Pro Pro Ala
          275          280          285
Leu Glu Lys Lys Tyr Gln Leu Asn Leu Pro Pro Tyr Pro Asp Thr
          290          295          300
Glu Cys Val Tyr Arg Leu Gln
          305

```

<210> 4

<211> 402

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID NO: 1648214CD1

<400> 4

Met	Met	Val	Ala	Leu	Arg	Gly	Ala	Ser	Ala	Leu	Leu	Val	Leu	Phe	1	5	10	15
Leu	Ala	Ala	Phe	Leu	Pro	Pro	Pro	Gln	Cys	Ala	Gln	Asp	Pro	Ala	20	25	30	
Met	Val	His	Tyr	Ile	Tyr	Gln	Arg	Phe	Arg	Val	Leu	Glu	Gln	Gly	35	40	45	
Leu	Glu	Lys	Cys	Thr	Gln	Ala	Thr	Arg	Ala	Tyr	Ile	Gln	Glu	Phe	50	55	60	
Gln	Glu	Phe	Ser	Lys	Asn	Ile	Ser	Val	Met	Leu	Gly	Arg	Cys	Gln	65	70	75	
Thr	Tyr	Thr	Ser	Glu	Tyr	Lys	Ser	Ala	Val	Gly	Asn	Leu	Ala	Leu	80	85	90	
Arg	Val	Glu	Arg	Ala	Gln	Arg	Glu	Ile	Asp	Tyr	Ile	Gln	Tyr	Leu	95	100	105	
Arg	Glu	Ala	Asp	Glu	Cys	Ile	Glu	Ser	Glu	Asp	Lys	Thr	Leu	Ala	110	115	120	
Glu	Met	Leu	Leu	Gln	Glu	Ala	Glu	Glu	Glu	Lys	Lys	Ile	Arg	Thr	125	130	135	
Leu	Leu	Asn	Ala	Ser	Cys	Asp	Asn	Met	Leu	Met	Gly	Ile	Lys	Ser	140	145	150	
Leu	Lys	Ile	Val	Lys	Lys	Met	Met	Asp	Thr	His	Gly	Ser	Trp	Met	155	160	165	
Lys	Asp	Ala	Val	Tyr	Asn	Ser	Pro	Lys	Val	Tyr	Leu	Leu	Ile	Gly	170	175	180	
Ser	Arg	Asn	Asn	Thr	Val	Trp	Glu	Phe	Ala	Asn	Ile	Arg	Ala	Phe	185	190	195	
Met	Glu	Asp	Asn	Thr	Lys	Pro	Ala	Pro	Arg	Lys	Gln	Ile	Leu	Thr	200	205	210	
Leu	Ser	Trp	Gln	Gly	Thr	Gly	Gln	Val	Ile	Tyr	Lys	Gly	Phe	Leu	215	220	225	
Phe	Phe	His	Asn	Gln	Ala	Thr	Ser	Asn	Glu	Ile	Ile	Lys	Tyr	Asn	230	235	240	
Leu	Gln	Lys	Arg	Thr	Val	Glu	Asp	Arg	Met	Leu	Leu	Pro	Gly	Gly	245	250	255	
Val	Gly	Arg	Ala	Leu	Val	Tyr	Gln	His	Ser	Pro	Ser	Thr	Tyr	Ile	260	265	270	
Asp	Leu	Ala	Val	Asp	Glu	His	Gly	Leu	Trp	Ala	Ile	His	Ser	Gly	275	280	285	
Pro	Gly	Thr	His	Ser	His	Leu	Val	Leu	Thr	Lys	Ile	Glu	Pro	Gly	290	295	300	
Thr	Leu	Gly	Val	Glu	His	Ser	Trp	Asp	Thr	Pro	Cys	Arg	Ser	Gln	305	310	315	
Asp	Ala	Glu	Ala	Ser	Phe	Leu	Leu	Cys	Gly	Val	Leu	Tyr	Val	Val	320	325	330	
Tyr	Ser	Thr	Gly	Gly	Gln	Gly	Pro	His	Arg	Ile	Thr	Cys	Ile	Tyr	335	340	345	
Asp	Pro	Leu	Gly	Thr	Ile	Ser	Glu	Glu	Asp	Leu	Pro	Asn	Leu	Phe	350	355	360	
Phe	Pro	Lys	Arg	Pro	Arg	Ser	His	Ser	Met	Ile	His	Tyr	Asn	Pro	365	370	375	
Arg	Asp	Lys	Gln	Leu	Tyr	Ala	Trp	Asn	Glu	Gly	Asn	Gln	Ile	Thr	380	385	390	
Tyr	Lys	Leu	Gln	Thr	Lys	Arg	Lys	Leu	Pro	Leu	Lys				395	400		

<210> 5
 <211> 409
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID NO: 2743295CD1

<400> 5
 Met Thr Ser Val Thr Arg Thr Ala Cys Ser His Pro Ser Gly His
 1 5 10 15
 Ser Thr Ala Val Thr Ser Asp Leu Asn Ala Arg Thr Ala Pro Trp
 20 25 30
 Ser Ser Ala Leu Pro Gln Pro Ser Thr Ser Asp Pro Ser Ile Ala
 35 40 45
 Asn His Ala Ser Val Gly Pro Thr Leu Gln Thr Thr Ser Val Ser
 50 55 60
 Pro Asp Pro Thr Arg Glu Ser Val Leu Gln Pro Ser Pro Gln Val
 65 70 75
 Pro Ala Thr Thr Val Ala His Thr Ala Thr Gln Gln Pro Ala Ala
 80 85 90
 Pro Ala Pro Pro Ala Val Ser Pro Arg Glu Ala Leu Met Glu Ala
 95 100 105
 Met His Thr Val Pro Val Pro Pro Thr Thr Val Arg Thr Asp Ser
 110 115 120
 Leu Gly Lys Asp Ala Pro Ala Gly Trp Gly Thr Thr Pro Ala Ser
 125 130 135
 Pro Thr Leu Ser Pro Glu Glu Glu Asp Asp Ile Arg Asn Val Ile
 140 145 150
 Gly Arg Cys Lys Asp Thr Leu Ser Thr Ile Thr Gly Pro Thr Thr
 155 160 165
 Gln Asn Thr Tyr Gly Arg Asn Glu Gly Ala Trp Met Lys Asp Pro
 170 175 180
 Leu Ala Lys Asp Glu Arg Ile Tyr Val Thr Asn Tyr Tyr Tyr Gly
 185 190 195
 Asn Thr Leu Val Glu Phe Arg Asn Leu Glu Asn Phe Lys Gln Gly
 200 205 210
 Arg Trp Ser Asn Ser Tyr Lys Leu Pro Tyr Ser Trp Ile Gly Thr
 215 220 225
 Gly His Val Val Tyr Asn Gly Ala Phe Tyr Tyr Asn Arg Ala Phe
 230 235 240
 Thr Arg Asn Ile Ile Lys Tyr Asp Leu Lys Gln Arg Tyr Val Ala
 245 250 255
 Ala Trp Ala Met Leu His Asp Val Ala Tyr Glu Glu Ala Thr Pro
 260 265 270
 Trp Arg Trp Gln Gly His Ser Asp Val Asp Phe Ala Val Asp Glu
 275 280 285
 Asn Gly Leu Trp Leu Ile Tyr Pro Ala Leu Asp Asp Glu Gly Phe
 290 295 300
 Ser Gln Glu Val Ile Val Leu Ser Lys Leu Asn Ala Ala Asp Leu
 305 310 315
 Ser Thr Gln Lys Glu Thr Thr Trp Arg Thr Gly Leu Arg Arg Asn
 320 325 330
 Phe Tyr Gly Asn Cys Phe Val Ile Cys Gly Val Leu Tyr Ala Val
 335 340 345
 Asp Ser Tyr Asn Gln Arg Asn Ala Asn Ile Ser Tyr Ala Phe Asp

	350		355		360
Thr His Thr Asn Thr Gln Ile Val Pro Arg Leu Leu Phe Glu Asn					
	365		370		375
Glu Tyr Ser Tyr Thr Thr Gln Ile Asp Tyr Asn Pro Lys Asp Arg					
	380		385		390
Leu Leu Tyr Ala Trp Asp Asn Gly His Gln Val Thr Tyr His Val					
	395		400		405
Ile Phe Ala Tyr					

<210> 6

<211> 271

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID NO: 2821011CD1

<400> 6

Met Arg Gly Asn Leu Ala Leu Val Gly Val Leu Ile Ser Leu Ala		
1	5	10
Phe Leu Ser Leu Leu Pro Ser Gly His Pro Gln Pro Ala Gly Asp		
	20	25
Asp Ala Cys Ser Val Gln Ile Leu Val Pro Gly Leu Lys Gly Asp		
	35	40
Ala Gly Glu Lys Gly Asp Lys Gly Ala Pro Gly Arg Pro Gly Arg		
	50	55
Val Gly Pro Thr Gly Glu Lys Gly Asp Met Gly Asp Lys Gly Gln		
	65	70
Lys Gly Ser Val Gly Arg His Gly Lys Ile Gly Pro Ile Gly Ser		
	80	85
Lys Gly Glu Lys Gly Asp Ser Gly Asp Ile Gly Pro Pro Gly Pro		
	95	100
Asn Gly Glu Pro Gly Leu Pro Cys Glu Cys Ser Gln Leu Arg Lys		
	110	115
Ala Ile Gly Glu Met Asp Asn Gln Val Ser Gln Leu Thr Ser Glu		
	125	130
Leu Lys Phe Ile Lys Asn Ala Val Ala Gly Val Arg Glu Thr Glu		
	140	145
Ser Lys Ile Tyr Leu Leu Val Lys Glu Glu Lys Arg Tyr Ala Asp		
	155	160
Ala Gln Leu Ser Cys Gln Gly Arg Gly Gly Thr Leu Ser Met Pro		
	170	175
Lys Asp Glu Ala Ala Asn Gly Leu Met Ala Ala Tyr Leu Ala Gln		
	185	190
Ala Gly Leu Ala Arg Val Phe Ile Gly Ile Asn Asp Leu Glu Lys		
	200	205
Glu Gly Ala Phe Val Tyr Ser Asp His Ser Pro Met Arg Thr Phe		
	215	220
Asn Lys Trp Arg Ser Gly Glu Pro Asn Asn Ala Tyr Asp Glu Glu		
	230	235
Asp Cys Val Glu Met Val Ala Ser Gly Gly Trp Asn Asp Val Ala		
	245	250
Cys His Thr Thr Met Tyr Phe Met Cys Glu Phe Asp Lys Glu Asn		
	260	265
Met		270

<210> 7
 <211> 325
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte ID NO: 2921920CD1

<400> 7

Met	Leu	Ser	Met	Leu	Arg	Thr	Met	Thr	Arg	Leu	Cys	Phe	Leu	Leu
1				5					10					15
Phe	Phe	Ser	Val	Ala	Thr	Ser	Gly	Cys	Ser	Ala	Ala	Ala	Ala	Ser
				20					25					30
Ser	Leu	Glu	Met	Leu	Ser	Arg	Glu	Phe	Glu	Thr	Cys	Ala	Phe	Ser
				35					40					45
Phe	Ser	Ser	Leu	Pro	Arg	Ser	Cys	Lys	Glu	Ile	Lys	Glu	Arg	Cys
				50					55					60
His	Ser	Ala	Gly	Asp	Gly	Leu	Tyr	Phe	Leu	Arg	Thr	Lys	Asn	Gly
				65					70					75
Val	Val	Tyr	Gln	Thr	Phe	Cys	Asp	Met	Thr	Ser	Gly	Gly	Gly	Gly
				80					85					90
Trp	Thr	Leu	Val	Ala	Ser	Val	His	Glu	Asn	Asp	Met	His	Gly	Lys
				95					100					105
Cys	Thr	Val	Gly	Asp	Arg	Trp	Ser	Ser	Gln	Gln	Gly	Asn	Lys	Ala
				110					115					120
Asp	Tyr	Pro	Glu	Gly	Asp	Gly	Asn	Trp	Ala	Asn	Tyr	Asn	Thr	Phe
				125					130					135
Gly	Ser	Ala	Glu	Ala	Ala	Thr	Ser	Asp	Asp	Tyr	Lys	Asn	Pro	Gly
				140					145					150
Tyr	Tyr	Asp	Ile	Gln	Ala	Lys	Asp	Leu	Gly	Ile	Trp	His	Val	Pro
				155					160					165
Asn	Lys	Ser	Pro	Met	Gln	His	Trp	Arg	Asn	Ser	Ala	Leu	Leu	Arg
				170					175					180
Tyr	Arg	Thr	Asn	Thr	Gly	Phe	Leu	Gln	Arg	Leu	Gly	His	Asn	Leu
				185					190					195
Phe	Gly	Ile	Tyr	Gln	Lys	Tyr	Pro	Val	Lys	Tyr	Arg	Ser	Gly	Lys
				200					205					210
Cys	Trp	Asn	Asp	Asn	Gly	Pro	Ala	Ile	Pro	Val	Val	Tyr	Asp	Phe
				215					220					225
Gly	Asp	Ala	Lys	Lys	Thr	Ala	Ser	Tyr	Tyr	Ser	Pro	Tyr	Gly	Gln
				230					235					240
Arg	Glu	Phe	Val	Ala	Gly	Phe	Val	Gln	Phe	Arg	Val	Phe	Asn	Asn
				245					250					255
Glu	Arg	Ala	Ala	Asn	Ala	Leu	Cys	Ala	Gly	Ile	Lys	Val	Thr	Gly
				260					265					270
Cys	Asn	Thr	Glu	His	His	Cys	Ile	Gly	Gly	Gly	Gly	Phe	Phe	Pro
				275					280					285
Gln	Gly	Lys	Pro	Arg	Gln	Cys	Gly	Asp	Phe	Ser	Ala	Phe	Asp	Trp
				290					295					300
Asp	Gly	Tyr	Gly	Thr	His	Val	Lys	Ser	Ser	Cys	Ser	Arg	Glu	Ile
				305					310					315
Thr	Glu	Ala	Ala	Val	Leu	Leu	Phe	Tyr	Arg					
				320					325					

<210> 8
 <211> 3519
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <223> Incyte ID NO: 714029CB1

<400> 8
 gcgcgcgcgcg tcccacgtac cccgcgcgcgc cgggcaagaa gatggcggga tcagtggccg 60
 acagcaatgc cgtgggtgaaa ctatagatgat gccattttaa caactctttg agctctccag 120
 ttcaagcggga cgtgtacttc ccacgactga tagttccatt ttgtgggcac attaaagggtg 180
 gcatgagacc aggcaagaag gtgttagtga tgggcatcgt agacctcaac ccagagagct 240
 ttgcaatcag cttgacctgt ggggactcag aagacctcc tgcgatgtg gcaatcgaac 300
 tcaaagctgt gttcacagat cggcagctac tcagaaatc ttgtatatct ggggagagggt 360
 gtgaagaaca gtcagcaatc ccttactttc cattcattcc agaccagcca ttcagggtgg 420
 aaattctttg tgagcaccca cgtttccgag tgtttgtgga tggacaccaa ctttttgatt 480
 ttaccatcg cattcaaacg ttatctgcaa ttgacaccat aaagataaat ggagacctcc 540
 agatcaccaa gcttggctga tttaaaccac ctctatttca aataggatca cgtgccacaa 600
 ctatctgact gttggctctgg aagaagtgtc ctgcaagat ctggagactt aaaaagaaaa 660
 caaaaacaaa tggcaagttt cacttaagggt tggtttgccc ttaagaagaa agctgttggg 720
 acaagacac cgagccatta taccagaat aaaataatac atttatgctg gattttattc 780
 agaccaaact aaaatggatt tgtgatgatt tgtgatttgg tagcaaatta ttcattcttt 840
 caaagcaagg caatgcttag aaacagaagt gctaaagaca cttaaaaagc caacaacaac 900
 ggtacagtga aatcaatgca tttctgcact aaagtggaa tgtgtagcac aaccaatatt 960
 ttagtcagggt tatttacata gaatgtagggt tgttcaagggt ttgacttttt ttttgttttt 1020
 tgtttttgtt tttgtttttg ttttgcacag cataatgtta attcagattg ttgaagcttt 1080
 cttgtagtta tttatttata ctcaatgtat gtattaaaga atgaacaatg tctcaagaac 1140
 agcaagttgt aaacttttga atgtataaat atcttaggtc caaggggaga aaattacata 1200
 ttacaattat gaaacaggtg aatttctgct ttaaagaatt gagattctcc ataccctaa 1260
 acttaggatc tcttgatata aactgctgta agtgcttttg ggaaaccttt gcaaaaccat 1320
 tttgataaaa ctgctttcca agttattgtt ggttatgtaa aattctattt acattgcttt 1380
 ttctccttac tgggaattag cacattattg gcttccttaa gactaattat ttctctcttg 1440
 atttatataa tagctcatta agttgttatt aatcaaaaaac acaaagaggt gattgcttag 1500
 acaattttta agtgactat agtataaact tttaaaagaa taatatgaaa atgactgtgg 1560
 aatgcagtgt aaagcagaag caaacggccc tgaataactt acttggaggt aatttatatc 1620
 aacttaagct gttagctcat tgtataactt ttcttatgtg acctcacca atatccctaa 1680
 gtaatgcctt tgggaagctt agagtagaag atgcttccca ctgtgttggc tctgaggaga 1740
 tagtaggatt agataggatc cagattagga aatgatccag ttagtttatc tgaaagggtta 1800
 actcccagga ctccaggtct ttgaatccag ccagtagagt gaatgcttcc aattaagctg 1860
 taggtgttac cctgcactta cggaaactgat caaacagggt actccaacag gaggttgacg 1920
 tactgtaaac gtcaccgcaa ggcaagggtat gcttaaagtc ctgggttctg gactttaaaa 1980
 gctacattgg ccctggagggt agggaccctt ggcatgtctt tgatcaggta gtgagggaag 2040
 acagggttct ggggtggggg tgtatttata tataatttag gttttgtttg tacagcatac 2100
 tgtgtcttgt aatgacacat ccttgccttg ctttcccttt ttgagttttt tttttttttt 2160
 tacacaacat gcagaggcgc tgaagtgaac atgtcatttt caagtgtcaa gaatgtagac 2220
 agtgtttcag taccaaaagtc taaaataaac taaaattatg aattttttat aggtgatata 2280
 tttggattct tctcaacttt gaaactgttt agcacagttc cattgtatta tataagaaga 2340
 cactgtatcc aacaagactg gctgtacatt gaaaagcttt atgtaccagc caacttattt 2400
 aaccatattc agcctgttcc gtgggggctg ttctgtggtt ccagggtatt tcaagcctgt 2460
 gattaacttc tcatggcttg tcaactaaaa gtccctaaat ttgagagact taaagggcac 2520
 cttgaaatac atttgtggag ttttgatcca acttatgggt gaagagcccc atagggaagac 2580
 tgttttgagt ggccaacat tcccaccac tgcataattc agcagaaact agaggagcag 2640
 ggcgtgtact gattggaatt gacacgctta ttctgtctac ctatcagcta actcattagc 2700
 agccaagccc ttaggcagct tagtgtgaaa atacaatgtt aactgtttgt ttctctgtga 2760
 ggttagtggg aaccgcttgg ataagcctat tgggattaat ctaaatgatg tgatgatttg 2820


```

attcaggtat agcccaaatt agtaaggggc tttagctgta aactgaaaac aatattcaca 2880
ccctctcctg ggctgtgaag gtctaagggtg agaatttcag gatggaaaat gcaatgtaaa 2940
gcttccacag gaaagtattc gggtagttaa ggtgttattt ctgaccagag ccctagttct 3000
gcaataacca aaaccaagga gtataaataa caatcaggct ctgggggaat agaaagcagg 3060
ctttagacaa tctgtccatt tctacagtaa aattggagtg agtgtgtata tctacttaaa 3120
acttaataga agtgaacttct actttttggg ctattccaga agtattttaa aattattatt 3180
taaaattttg aagccccatt tcaaattctg ccgaccttag ttcaaagccc cctgagagat 3240
cacttttaga attgaggatt tgtaaaaatg gcaagtcatt tcatttgtgt taaaaagaaa 3300
atacccaaaa ggaaggaggg agccctgttt gccttgagat aaacggcctt ggcattttct 3360
ggcattaatg tagaaataat gtccctatga tgacatattt tcaaagaaac actttcttat 3420
ttactgtgtg gtgtaaaatg ttgctaaatg tgttgttaca ttatgtcact gctgaaagta 3480
atttgcacta taataaagga attttctaca aaaaaaaaaa 3519

```

<210> 9

<211> 2351

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID NO: 1450775CB1

<400> 9

```

ggagccggag gggcgcacac ttggagctga agccctctcc agggctccgg gccggtgccc 60
caacggacag aggtcgagga ggaccgcagc aggtggcagc ggccgggggc aggaggatgg 120
tgcagaagga gagtcaagcg acgttggagg agcgggagag cgagctcagc tccaaccctg 180
ccgcctctgc gggggcatcg ctggagccgc cggcagctcc ggcacccgga gaagacaacc 240
ccgccggggc tgggggagcg gcggtggccg gggctgcagg aggggctcgg cggttccctc 300
gcggtgtggt ggaaggattt tatggaagac ctctgggttat ggaacagaga aaagaactct 360
ttagaaggct ccagaaatgg gaattaaata catacttgta tgcccaaaa gatgactaca 420
aacataggat gttttggcga gagatgtatt cagtggagga agctgagcaa cttatgactc 480
tcctctctgc tgcacgagaa tatgagatag agttcatcta tgcgatctca cctggattgg 540
atatcacttt ttctaacccc aaggaagtat ccacattgaa acgtaaattg gaccagggtt 600
ctcagtttgg gtgcagatca tttgctttgc tttttgatga tatagaccat aatatgtgtg 660
cagcagacaa agaggttatc agttcttttg ctcatgccca agtctccatc acaaatgaaa 720
tctatcagta cctaggagag ccagaaactt tctctctctg tcccacagaa tactgtggca 780
ctttctgtta tccaaatgtg tctcagtcct catatttaag gactgtgggt gaaaagcttc 840
tacctggaat tgaagtgtt tggacagtc ccaaagtgtt ttctaaagaa attccagtag 900
agtccatcga agaggtttct aagattatta agagagctcc agtaatctgg gataacattc 960
atgctaatag ttatgatcag aagagactgt ttctggggcc gtacaaagga agatccacag 1020
aactcatccc acggttaaaa ggagtcctca ctaatccaaa ttgtgaattt gaagccaact 1080
acgttgctat ccacaccctt gccacctggt acaaatcaaa catgaatgga gtgagaaaag 1140
atgtagtgat gactgacagt gaagatagta ctgtgtccat ccagataaaa ttagaaaatg 1200
aaggcagtga tgaagatatt gaaactgatg tactctatag tccacagatg gctctaaagc 1260
tagcattaac agaatggttg caagagtttg gtgtgcctca tcaatacagc agtaggcaag 1320
ttgcacacag tggagctaaa gcaagtgtag ttgatgggac tcctttagtt gcagcaccct 1380
ctttaaatgc cacaaccgta gtaacaacag tttatcagga gccattatg agccaggag 1440
cagccttgag tggtagcct actactctga ccaaggaaaga agaaaagaaa cagcctgatg 1500
aagaacccat ggacatggtg gtggaaaaac aagaagaaac ggaccacaag aatgacaatc 1560
aaatactgag tgaattgtt gaagcgaaaa tggcagagga attgaaacca atggacactg 1620
ataaagagag catagctgaa tcaaaatccc cagagatgtc catgcaagaa gattgtatta 1680
gtgacattgc ccccatgcaa actgatgaac agacaaacaa ggagcagttt gtgccaggtc 1740
caaatgaaaa gcctttgtac actgcggaac cagtgaacct ggaggatttg cagttaactg 1800
ctgatctatt ctaccttctt tacgagcatg gacccaaagg agcacagatg ttacgggaat 1860
ttcaatggct tcgagcaaat agtagtgttg tcagtgtcaa ttgcaaagga aaagactctg 1920
aaaaaattga agaattggcg tcacgagcag ccaagtttga agagatgtgt ggactagtga 1980

```

```

tgggaatgtt cactcggctc tccaattgtg ccaacaggac aattctttat gacatgtact 2040
cctatgtttg ggatatcaag agtataatgt ctatggtgaa gtcttttgta cagtgggttag 2100
cgtttgctgc caattgatgg ggcaaatgat ctcttttttc agccacctcc actgactcct 2160
acctccaaag ttatactat cagaccttat tttcctaagg atgaggcatc cgtgtacaag 2220
atttgagag aaatgtatga cgatggagtg ggtttaccct ttcaaagtca acctgatctt 2280
attggagaca agttagtagg agggctgctt tccctcagcc tggattactg ctttgctcta 2340
gaagatgaag a
2351

```

<210> 10

<211> 1195

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID NO: 3369350CB1

<400> 10

```

ggcgagcgc cgcacatgcg ccggggcccg gccggggcccg gccggggcccg gggcgcgcg 60
tctgcgagct ggatgtccag gctgcggggcg ctgctggggc tcgggctgct ggttgcgggc 120
tcgcgcctgc cgcggatcaa aagccagacc atcgctgtc gctcgggacc cacctggtg 180
ggaccgcagc ggctgaactc ggggtggcgc tgggactcag aggtcatggc gagcacggtg 240
gtgaagtacc tgagccagga ggaggcccag gccgtggacc aggagctatt taacgaatac 300
cagttcagcg tggaccaact tatggaactg gccgggctga gctgtgctac agccatcgcc 360
aaggcatatc cccccacgct catgtccagg agcccccta ctgtcctggt catctgtggc 420
ccggggaata atggaggaga tgggtctggtc tgtgctcgac acctcaaact ctttggctac 480
gagccaacca tctattacce caaaaggcct aacaagcccc tcttactgct attggtgacc 540
cagtgtcaga aaatggacat ccctttcctt ggggaaatgc ccgcagagcc catgacgatt 600
gatgaactgt atgagctggt ggtggatgcc atctttggct tcagcttcaa gggcgatgtt 660
cgggaaccgt tccacagcat cctgagtgtc ctgaagggac tcaactgtgcc cattgccagc 720
atcgacattc cctcaggatg ggacgtggag aagggaaatg ctggagggat ccagccagac 780
ttgctcatct ccctcacagc cccccaaaaa tctgcaacce agtttaccgg tcgctaccat 840
tacctggggg gtcgttttgt gccacctgct ctggaaaaga agtaccagct gaacctgcca 900
ccctaccctg aactgagtg tgtctatcgt ctgcagtga ggaaggtggg tgggtattct 960
ccccataaaa gacttagagc ccctctcttc cagaactgtg gattcctggg agctcctctg 1020
gcaataaaaag tcagtgaatg gtggaagtca gagagcaacc ctggggattg ggtgccatct 1080
ctctaggggt aacacaaagg gcaagaggtt gctatggtat ttggaacaa tgaaaatgga 1140
ctggttagaaa aaaagaaaaa aaaaaaaaaa aaaaaaaaaa aaaagaagat cgaat 1195

```

<210> 11

<211> 2235

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID NO: 1648214CB1

<400> 11

```

ccccaggaag cagcttgcaa ccactagcct ggggagggtc cgcattgtgtc aagggtgagg 60
gcaacagatg ctggaccag ggagctctct gccacaggtc agtctacgag gcctcagga 120
ccaacttgcc aacagctgga cttgatcact agctggcaaa ctgagctcac gtatcgggtg 180
gaataacaag cggactttgc tctctgctgt gcaaaacgct gtttttagag gatttgccac 240
agcagcggat agagcaggag agcaccaccg gagcccttga gacatccttg agaagagcca 300
cagcataaga gactgccctg cttggtgttt tgcaggatga tggtgccct tcgaggagct 360

```

```

tctgcattgc tggttctggt ccttgacgct tttctgcccc egccgcagtg tgcccaggac 420
ccagccatgg tgcattacat ctaccagcgc tttcaggtct tggagcaagg gctggaaaaa 480
tgtacccaag caacgagggc atacattcaa gaattccaag agttctcaaa aaatatactt 540
gtcatgctgg gaagatgtca gacctacaca agtgagtaca agagtgcagt gggtaacttg 600
gcaactgagag ttgaacgtgc ccaacgggag attgactaca tacaatacct tcgagaggct 660
gacgagtgca tcgaatcaga ggacaagaca ctggcagaaa tggtgctcca agaagctgaa 720
gaagagaaaa agatccggac tctgctgaat gcaagctgtg acaacatgct gatgggcata 780
aagtctttga aaatagtga gaagatgatg gacacacatg gctcttgatg gaaagatgct 840
gtctataact ctccaaagggt gtacttatta attggatcca gaaacaacac tgtttgggaa 900
tttgcaaaac tacgggcatt catggaggat aacaccaagc cagctccccg gaagcaaate 960
ctaacacttt cctggcaggg aacaggccaa gtgatctaca aaggttttct attttttcat 1020
aaccaagcaa cttctaata gataatcaaa tataacctgc agaagaggac tgtggaagat 1080
cgaatgctgc tcccaggagg ggtaggccga gcattgggtt accagcactc cccctcaact 1140
tacattgacc tggctgtgga tgagcatggg ctctgggcca tccactctgg gccaggcacc 1200
catagccatt tggttctcac aaagattgag ccgggcacac tgggagtgga gcattcatgg 1260
gatacccat gcagaagcca ggatgctgaa gcctcattcc tcttggtggtg ggttctctat 1320
gtggtctaca gtactggggg ccagggccct catgcacat cctgcatcta tgatccactg 1380
ggcactatca gtgaggagga cttgcccac ttgttcttcc ccaagagacc aagaagtcac 1440
tccatgatcc attacaaccc cagagataag cagctctatg cctggaatga aggaaaccag 1500
atcacttaca aactccagac aaagagaaag ctgcctctga agtaatgcat tacagctgtg 1560
agaaagagca ctgtggcttt ggcatgctgt ctacaggaca gtgaggctat agccccctca 1620
caatatagta tccctctaact cacacacagg aagagtgtgt agaagtggaa atacgtatgc 1680
ctcctttccc aaatgtcact gccttaggta tcttccaaga gcttagatga gagcatatca 1740
tcaggaaagt ttcaacaatg tccattactc ccccaaact cctggctctc aaggatgacc 1800
acattctgat acagctact tcaagccttt tgttttactg ctccccagca tttactgtaa 1860
ctctgccatc ttccctccca caattagagt tgtatgccag cccctaatat tcaccactgg 1920
cttttctctc ccttggectt tgcgaagct ctccctctt tttcaaagt ctattgatat 1980
tctccattt tcaactgccc actaaaatac tattaatatt tctttctttt cttttctttt 2040
ttttgagaca agtctcact atgttgccc ggtggtctc aaactccaga gctcaagaga 2100
tcctctgccc tcagctcct aagtacctg gattacaggc atgtgccacc acacctggct 2160
taaaatacta tttcttattg aggtttaacc tctatttccc ctagecctgt ccttccacta 2220
agcttggtag atgta 2235

```

<210> 12

<211> 1877

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID NO:2743295CB1

<400> 12

```

tcccagccca ctgtcatccg gggcatcacc tactataaag ccaaggtctc tgaagaagag 60
aatgacattg aagagcagca agatgagttt ttcagcgggtg acaatggagt ggatttctg 120
attgaagatc agtccttgag acacaacggc ctgatgacca gtgtcaccgg gacggcctgc 180
agccaccctg caggacacag cactgctgtg acaagcgacc tgaacgctcg gaccgcaccc 240
tggctctcag cactgccaca gccctcgacc tcagatccca gcatcgccaa ccatgcctca 300
gtgggaccaa cactccaaac aacctcgggtg tctccagatc ccacaagggg gtcagtccctg 360
cagccttctc ctcaaggtacc agccaccact gtggccca cagccaccca gcaaccagca 420
gccccagctc ctccggcagt gtctcccagg gaggcattga tggaaagctat gcacacagtc 480
ccagtgcctc ccaccacagt cagaacagac tcgctgggga aagatgctcc tgctgggtgg 540
ggaacaaccc ctgccagccc cacgctgagc cccgaagaag aagatgacat ccggaatgtc 600
ataggaaggt gcaaggacac tctctccaca atcacggggc cgaccaccca gaacacatat 660
ggggggaatg aaggggctct gatgaaggac cccctggcca aggatgagcg gatttacgta 720
accaactatt actacggcaa caccctggta gagttccgga acctggagaa cttcaacaa 780

```

```

ggtcgctgga gcaattccta caagctcccg tacagctgga tcggcacagg ccacgtggta 840
tacaatggcg ccttctacta caatcgcgcc ttcaccgca acatcatcaa gtacgacctg 900
aagcagcgct acgtggctgc ctgggccatg ctgcatgacg tggcctacga ggaggccacc 960
ccctggcgat ggcagggccca ctgagacgtg gactttgctg tggacgagaa tggcctatgg 1020
ctcatctacc cggccctgga cgatgagggc ttcagccagg aggtcattgt cctgagcaag 1080
ctcaatgccg cggacctgag cacacagaag gagaccacat ggcgcacggg gctccggagg 1140
aatttctacg gcaactgctt cgtcatctgt ggggtgctgt atgccgtgga tagctacaac 1200
cagcgggaatg ccaacatctc ctacgcttcc gacaccacaca ccaacacaca gatcgctccc 1260
aggctgctgt tcgagaatga gtattcctat acgaccaga tagactacaa ccccaaggac 1320
cgctgctct atgcctggga caatggccac caggtcactt accatgtcat ctttgccctac 1380
tgacaccctt gtccccacaa gcagaagcac agaggggtca ctacgacctt gtgtgtatgt 1440
gtgtgcgcgc acgtgtgtgt aggtgggtat gtgtgtttta aaaatatata ttattttgta 1500
taatatgca aatgtaaaat gacaatttgg gtctattttt ttatatggat tgtagatcaa 1560
tcatacgtg tatgtgctgg tctcatctc cccagtttat atttttgtgc aaatgaactt 1620
ctccttttga ccagtaacca ccttcttca agccttcagc ccctccagct ccaagtctca 1680
gatctcgacc attgaaaagg tttcttcac tggttcttgc aggagggcagg caacaccagg 1740
agcagaaatg aaagaggcaa gaaagaagt ctatgtggcg agaaaaaaag ttttaatgta 1800
ttggagaagt tttaaaaaac ccagaaaaac gccttttttt ttaataaaag aagaaattta 1860
aatcaaaaaa aaaaaaa 1877

```

<210> 13

<211> 1253

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID NO: 2821011CB1

<400> 13

```

gggggcagtg tcctcgcggg ccagcgacgg gcaggacggc ccgttcgcct agcgcgctgct 60
caggagttgg tgctctgect gcgctcagga tgagggggaa tctggccctg gtgggcgttc 120
taatcagcct ggccttctcg tcaactgtgc catctggaca tcctcagccg gctggcgatg 180
acgcctgctc tgtgcagatc ctgcctcctg gctcaaaagg ggatgcggga gagaaggagg 240
acaaaggcgc ccccgacagg cctggaagag tcggcccccac gggagaaaaa ggagacatgg 300
gggacaaaagg acagaaaggc agtgtgggtc gtcattgaaa aattgggtccc attggctcta 360
aaggtgagaa aggagattcc ggtgacatag gacccctgg tcctaattga gaaccaggcc 420
tcccatgtga gtgcagccag ctgcgcaagg ccatcgggga gatggacaac caggctcttc 480
agctgaccag cgagctcaag ttcattcaaga atgtgtgcgc cgggtgtgcgc gagacggaga 540
gcaagatcta cctgctggtg aaggaggaga agcgctacgc ggacgcccag ctgtcctgcc 600
agggcgcggg gggcacgctg agcatgccc aggcaggggc tgccaatggc ctgatggccg 660
catacctggc gcaagccggc ctggcccgtg tcttcacgag catcaacgac ctggagaagg 720
agggcgcctt cgtgtactct gaccactccc ccatgcggac cttcaacaag tggcgacagg 780
gtgagcccaa caatgcctac gacgaggagg actgcgtgga gatgggtggc tcgggcggct 840
ggaacgacgt ggccctgcac accaccatgt acttcatgtg tgagtgtgac aaggagaaca 900
tgtgagcctc aggtggggc tgccattgg gggccccaca tgcctctgca ggggtggcag 960
ggacagagcc cagaccatgg tgccagccag ggagctgtcc ctctgtgaag ggtggaggct 1020
cactgagtag agggctgttg tctaaactga gaaaatggcc tatgtttaag aggaaaatga 1080
aagtgttctt ggggtgctgt ctctgaagaa gcagagtttc attacctgta ttgtagcccc 1140
aatgtcatta tgtaattatt acccagaatt gctcttccat aaagcttgtg cctttgtcca 1200
agctatacaa taaaatcttt aagtagtgca gtagttaagt ccaaaaaaaa aaa 1253

```

<210> 14

<211> 1142

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte ID NO: 2921920CB1

<400> 14

```

ggagctccga gtgtccacag gaaggggaact atcagctcct ggcactctgta aggatgctgt 60
ccatgctgag gacaatgacc agactctgct tcctgttatt cttctctgtg gccaccagtg 120
ggtgccagtgc agcagcagcc tcttctcttg agatgctctc gaggggaattc gaaacctgtg 180
ccttctcctt ttcttccctg cctagaagct gcaaagaaat caaggaacgc tgccatagtg 240
caggtgatgg cctgtathtt ctccgcacca agaatggtgt tgtctaccag accttctgtg 300
acatgacttc tgggggtggc ggctggaccc tgggtggccag cgtgcacgag aatgacatgc 360
atgggaagtg cacggtgggt gatcgctggt ccagtcagca gggcaacaaa gcagactacc 420
cagaggggga tggcaactgg gccaactaca acacctttgg atctgcagag gcggccacga 480
gcatgacta caagaacctt ggctactacg acatccaggc caaggacctg ggcactctgc 540
atgtgcccac caagtcccc atgcagcatt ggagaaacag cgccctgctg aggtaccgca 600
ccaacactgg cttcctccag agactgggac ataatctgtt tggcatctac cagaaatacc 660
cagtgaata cagatcaggg aaatgttggg atgacaatgg cccagccata cctgtggtct 720
atgactttgg tggatgctaag aagactgcat cttattactc accgtatggt caacgggaat 780
ttgttgcagg attcgttcag ttccgggtgt ttaataacga gagagcagc aacgcccttt 840
gtgctgggat aaaagttact ggctgtaaca ctgagcatca ctgcatcggg ggaggagggt 900
tcttcccaca gggcaaaccc cgtcagtgtg gggacttctc cgcctttgac tgggatggat 960
atggaactca cgttaagagc agctgcagtc gggagataac ggaggcggct gtactcttgt 1020
tctatagatg agacagagct ctgcggtgtc agggcgagaa cccatcttcc aaccccggt 1080
atgtggagac ggaaaaactg gaattctaac aaggaggaga ggagactaaa tcacatcaat 1140
tc

```

1142

<210> 15

<211> 316

<212> PRT

<213> Homo sapiens

<300>

<308> g2810994

<400> 15

```

Met Leu Ser Leu Asn Asn Leu Gln Asn Ile Ile Tyr Asn Pro Val
  1          5          10          15
Ile Pro Phe Val Gly Thr Ile Pro Asp Gln Leu Asp Pro Gly Thr
          20          25          30
Leu Ile Val Ile Arg Gly His Val Pro Ser Asp Ala Asp Arg Phe
          35          40          45
Gln Val Asp Leu Gln Asn Gly Ser Ser Val Lys Pro Arg Ala Asp
          50          55          60
Val Ala Phe His Phe Asn Pro Arg Phe Lys Arg Ala Gly Cys Ile
          65          70          75
Val Cys Asn Thr Leu Ile Asn Glu Lys Trp Gly Arg Glu Glu Ile
          80          85          90
Thr Tyr Asp Thr Pro Phe Lys Arg Glu Lys Ser Phe Glu Ile Val
          95          100          105
Ile Met Val Leu Lys Asp Lys Phe Gln Val Ala Val Asn Gly Lys
          110          115          120
His Thr Leu Leu Tyr Gly His Arg Ile Gly Pro Glu Lys Ile Asp
          125          130          135

```

Thr	Leu	Gly	Ile	Tyr	Gly	Lys	Val	Asn	Ile	His	Ser	Ile	Gly	Phe	
				140					145					150	
Ser	Phe	Ser	Ser	Asp	Leu	Gln	Ser	Thr	Gln	Ala	Ser	Ser	Leu	Glu	
				155					160					165	
Leu	Thr	Glu	Ile	Val	Arg	Glu	Asn	Val	Pro	Lys	Ser	Gly	Thr	Pro	
				170					175					180	
Gln	Leu	Ser	Leu	Pro	Phe	Ala	Ala	Arg	Leu	Asn	Thr	Pro	Met	Gly	
				185					190					195	
Pro	Gly	Arg	Thr	Val	Val	Val	Gln	Gly	Glu	Val	Asn	Ala	Asn	Ala	
				200					205					210	
Lys	Ser	Phe	Asn	Val	Asp	Leu	Leu	Ala	Gly	Lys	Ser	Lys	Asp	Ile	
				215					220					225	
Ala	Leu	His	Leu	Asn	Pro	Arg	Leu	Asn	Ile	Lys	Ala	Phe	Val	Arg	
				230					235					240	
Asn	Ser	Phe	Leu	Gln	Glu	Ser	Trp	Gly	Glu	Glu	Glu	Arg	Asn	Ile	
				245					250					255	
Thr	Ser	Phe	Pro	Phe	Ser	Pro	Gly	Met	Tyr	Phe	Glu	Met	Ile	Ile	
				260					265					270	
Tyr	Cys	Asp	Val	Arg	Glu	Phe	Lys	Val	Ala	Val	Asn	Gly	Val	His	
				275					280					285	
Ser	Leu	Glu	Tyr	Lys	His	Arg	Phe	Lys	Glu	Leu	Ser	Ser	Ile	Asp	
				290					295					300	
Thr	Leu	Glu	Ile	Asn	Gly	Asp	Ile	His	Leu	Leu	Glu	Val	Arg	Ser	
				305					310					315	

Trp

<210> 16

<211> 1042

<212> PRT

<213> Clostridium perfringens

<300>

<308> g144861

<400> 16

Met	Asn	Lys	Asn	Ile	Arg	Lys	Ile	Ile	Thr	Ser	Thr	Val	Leu	Ala	
1				5					10					15	
Ala	Met	Thr	Ile	Ser	Val	Leu	Pro	Ser	Asn	Leu	Val	Val	Phe	Ala	
				20					25					30	
Thr	Asp	Gly	Ile	Thr	Glu	Asn	Phe	Tyr	Glu	Ile	Tyr	Pro	Lys	Pro	
				35					40					45	
Gln	Glu	Ile	Ser	Tyr	Ser	Gly	Gly	Glu	Phe	Gln	Ile	Ser	Asp	Glu	
				50					55					60	
Ile	Asn	Ile	Val	Tyr	Asp	Asp	Gly	Ile	Asp	Thr	Tyr	Thr	Lys	Lys	
				65					70					75	
Arg	Val	Asp	Glu	Val	Leu	Glu	Ala	Ser	Asn	Leu	Glu	Ala	Thr	Val	
				80					85					90	
Ser	Asn	Glu	Ile	Val	Pro	Gly	Lys	Thr	Asn	Phe	Leu	Val	Gly	Ile	
				95					100					105	
Asn	Glu	Ser	Gly	Gly	Val	Val	Asp	Asn	Tyr	Phe	Asn	Lys	Asn	Ile	
				110					115					120	
Pro	His	Asp	Glu	Ser	Phe	Phe	Asp	Glu	Lys	Met	Asp	Ala	Asn	Ile	
				125					130					135	
Val	Ser	Val	Lys	Asp	Gly	Val	Ile	Gly	Val	Ile	Ala	Glu	Asp	Thr	
				140					145					150	

Asp Ser Ala Phe Tyr Gly Val Thr Thr	Leu Lys His Val Phe Asn	155	160	165
Gln Leu Glu Glu Gly Asn Glu Ile Lys	Asn Phe Arg Ala Asp Asp	170	175	180
Tyr Ala Glu Val Ala His Arg Gly Phe	Ile Glu Gly Tyr Tyr Gly	185	190	195
Asn Pro Trp Ser Asn Glu Asp Arg Ala	Glu Leu Met Lys Phe Gly	200	205	210
Gly Asp Tyr Lys Leu Asn Gln Tyr Val	Phe Ala Pro Lys Asp Asp	215	220	225
Pro Tyr His Asn Ser Lys Trp Arg Asp	Leu Tyr Pro Glu Glu Lys	230	235	240
Leu Ser Glu Ile Lys Lys Leu Ala Gln	Met Gly Asn Glu Thr Lys	245	250	255
Asn Arg Tyr Val Tyr Ala Leu His Pro	Phe Met Asn Asn Pro Val	260	265	270
Arg Phe Asp Thr Glu Glu Asn Tyr Gln	Asn Asp Leu Gly Val Ile	275	280	285
Lys Ala Lys Phe Thr Gln Leu Leu Glu	Asn Asp Val Arg Gln Phe	290	295	300
Ala Ile Leu Ala Asp Asp Ala Ser Ala	Pro Ala Gln Gly Ala Ser	305	310	315
Met Tyr Val Lys Leu Leu Thr Asp Leu	Thr Arg Trp Leu Glu Glu	320	325	330
Gln Gln Ser Thr Tyr Pro Asp Leu Lys	Thr Asp Leu Met Phe Cys	335	340	345
Pro Ser Asp Tyr Tyr Gly Asn Gly Ser	Ser Ala Gln Leu Lys Glu	350	355	360
Leu Asn Lys Ala Glu Asp Asn Val Ser	Ile Val Met Thr Gly Gly	365	370	375
Arg Ile Trp Gly Glu Val Asp Glu Asn	Phe Asn Phe Met			390
Asn Asn Ile Ser Thr Glu Gly His Pro	Gly Arg Ala Pro Phe Phe	395	400	405
Trp Ile Asn Trp Pro Cys Ser Asp Asn	Ser Lys Gln His Leu Ile	410	415	420
Met Gly Gly Asn Asp Thr Phe Leu His	Pro Gly Val Asp Pro Ser	425	430	435
Lys Ile Asp Gly Ile Val Leu Asn Pro	Met Gln Gln Ala Glu Ala	440	445	450
Asn Lys Ser Ala Leu Phe Ala Ile Ala	Asp Tyr Ala Trp Asn Ile	455	460	465
Trp Asp Asn Lys Glu Glu Ala Asp Glu	Asn Trp Asn Asp Ser Phe	470	475	480
Lys Tyr Met Asp His Gly Thr Ala Glu	Glu Thr Asn Ser Ser Leu	485	490	495
Ala Leu Arg Glu Ile Ser Lys His Met	Ile Asn Gln Asn Met Asp	500	505	510
Gly Arg Val Arg Pro Leu Gln Glu Ser	Val Glu Leu Ala Pro Lys	515	520	525
Leu Glu Ala Phe Lys Gln Lys Tyr Asp	Ser Gly Ala Ser Ile Lys	530	535	540
Glu Asp Ala Leu Glu Leu Ile Glu Glu	Phe Thr Asn Leu Gln Lys	545	550	555
Ala Ala Glu Tyr Tyr Lys Asn Asn Pro	Gly Asn Glu Arg Thr Arg	560	565	570
Asp Gln Ile Ile Tyr Trp Leu Asn Cys	Trp Glu Asp Thr Met Asp			

	575	580	585
Ala Ala Ile Gly Tyr Leu Lys Ser Ala	Ile Ala Ile Glu Glu Gly		
590	595	600	
Asp Asp Glu Ala Ala Trp Ala Asn Tyr	Ser Glu Ala Gln Ser Ala		
605	610	615	
Phe Glu Lys Ser Lys Thr Tyr Gly Phe	His Tyr Val Asp His Thr		
620	625	630	
Glu Tyr Ala Glu Val Gly Val Gln His	Ile Val Pro Phe Ile Lys		
635	640	645	
Ser Met Gly Gln Asn Leu Ser Val Val	Ile Gly Ser Ile Val Asp		
650	655	660	
Pro Asn Arg Ile Ile Ala Thr Tyr Ile	Ser Asn Arg Gln Asp Ala		
665	670	675	
Pro Thr Gly Asn Pro Asp Asn Ile Phe	Asp Asn Asn Ala Ser Thr		
680	685	690	
Glu Leu Val Tyr Lys Asn Pro Asn Arg	Ile Asp Val Gly Thr Tyr		
695	700	705	
Val Gly Val Lys Tyr Ser Asn Pro Ile	Thr Leu Asn Asn Val Glu		
710	715	720	
Phe Leu Met Gly Ala Asn Ser Asn Pro	Asn Asp Thr Met Gln Lys		
725	730	735	
Ala Lys Ile Gln Tyr Thr Val Asp Gly	Arg Glu Trp Ile Asp Leu		
740	745	750	
Glu Glu Gly Val Glu Tyr Thr Met Pro	Gly Ala Ile Lys Val Glu		
755	760	765	
Asn Leu Asp Leu Lys Val Arg Gly Val	Arg Leu Ile Ala Thr Glu		
770	775	780	
Ala Arg Glu Asn Thr Trp Leu Gly Val	Arg Asp Ile Asn Val Asn		
785	790	795	
Lys Lys Glu Asp Ser Asn Ser Gly Val	Glu Phe Asn Pro Ser Leu		
800	805	810	
Ile Arg Ser Glu Ser Trp Gln Val Tyr	Glu Gly Asn Glu Ala Asn		
815	820	825	
Leu Leu Asp Gly Asp Asp Asn Thr Gly	Val Trp Tyr Lys Thr Leu		
830	835	840	
Asn Gly Asp Thr Ser Leu Ala Gly Glu	Phe Ile Gly Leu Asp Leu		
845	850	855	
Gly Lys Glu Ile Lys Leu Asp Gly Ile	Arg Phe Val Ile Gly Lys		
860	865	870	
Asn Gly Gly Gly Ser Ser Asp Lys Trp	Asn Lys Phe Lys Leu Glu		
875	880	885	
Tyr Ser Leu Asp Asn Glu Ser Trp Thr	Thr Ile Lys Glu Tyr Asp		
890	895	900	
Lys Thr Gly Ala Pro Ala Gly Lys Asp	Val Ile Glu Glu Ser Phe		
905	910	915	
Glu Thr Pro Ile Ser Ala Lys Tyr Ile	Arg Leu Thr Asn Met Glu		
920	925	930	
Asn Ile Asn Lys Trp Leu Thr Phe Ser	Glu Phe Ala Ile Val Ser		
935	940	945	
Asp Glu Leu Glu Ser Ala Gly Asn Lys	Glu Asn Val Tyr Thr Asn		
950	955	960	
Thr Glu Leu Asp Leu Leu Ser Leu Ala	Lys Glu Asp Val Thr Lys		
965	970	975	
Leu Ile Pro Ile Asp Asp Leu Ser Leu	Asn His Gly Glu Tyr Ile		
980	985	990	
Gly Val Lys Leu Asn Arg Ile Lys Asp	Leu Ser Asn Ile Asn Leu		
995	1000	1005	

Glu Ile Ser Asn Asp Thr Gly Leu Lys Leu Gln Ser Ser Met Asn
 1010 1015 1020

Gly Val Glu Trp Thr Glu Ile Thr Asp Lys Asn Thr Leu Glu Asp
 1025 1030 1035

Gly Arg Tyr Val Arg Leu Phe
 1040

<210> 17

<211> 97

<212> PRT

<213> Homo sapiens

<300>

<308> g1247124

<400> 17

Gly Pro Thr Val Leu Val Ile Cys Gly Pro Gly Asn Asn Gly Gly
 1 5 10 15
 Asp Gly Leu Val Cys Ala Arg His Leu Lys Leu Phe Gly Tyr Glu
 20 25 30
 Pro Thr Ile Tyr Tyr Pro Lys Arg Pro Asn Lys Pro Leu Phe Thr
 35 40 45
 Ala Leu Val Thr Gln Cys Gln Lys Met Asp Ile Pro Phe Leu Gly
 50 55 60
 Glu Met Pro Ala Glu Pro Met Thr Ile Asp Glu Leu Tyr Glu Leu
 65 70 75
 Val Val Asp Ala Ile Phe Gly Phe Ser Phe Lys Gly Asp Val Arg
 80 85 90
 Glu Pro Phe His Val Pro Ser
 95

<210> 18

<211> 457

<212> PRT

<213> Rattus norvegicus

<300>

<308> g442368

<400> 18

Met Gln Pro Ala Arg Lys Leu Leu Ser Leu Leu Val Leu Leu Val
 1 5 10 15
 Met Gly Thr Glu Leu Thr Gln Val Leu Pro Thr Asn Pro Glu Glu
 20 25 30
 Ser Trp Gln Val Tyr Ser Ser Ala Gln Asp Ser Glu Gly Arg Cys
 35 40 45
 Ile Cys Thr Val Val Ala Pro Gln Gln Thr Met Cys Ser Arg Asp
 50 55 60
 Ala Arg Thr Lys Gln Leu Arg Gln Leu Leu Glu Lys Val Gln Asn
 65 70 75
 Met Ser Gln Ser Ile Glu Val Leu Asp Arg Arg Thr Gln Arg Asp
 80 85 90
 Leu Gln Tyr Val Glu Lys Met Glu Asn Gln Met Lys Gly Leu Glu

	95	100	105
Ser Lys Phe Arg	Gln Val Glu Glu Ser	His Lys Gln His Leu	Ala
	110	115	120
Arg Gln Phe Lys	Ala Ile Lys Ala Lys	Met Asp Glu Leu Arg	Pro
	125	130	135
Leu Ile Pro Val	Leu Glu Glu Tyr Lys	Ala Asp Ala Lys Leu	Val
	140	145	150
Leu Gln Phe Lys	Glu Glu Val Gln Asn	Leu Thr Ser Val Leu	Asn
	155	160	165
Glu Leu Gln Glu	Glu Ile Gly Ala Tyr	Asp Tyr Asp Glu Leu	Gln
	170	175	180
Ser Arg Val Ser	Asn Leu Glu Glu Arg	Leu Arg Ala Cys Met	Gln
	185	190	195
Lys Leu Ala Cys	Gly Lys Leu Thr Gly	Ile Ser Asp Pro Val	Thr
	200	205	210
Val Lys Thr Ser	Gly Ser Arg Phe Gly	Ser Trp Met Thr Asp	Pro
	215	220	225
Leu Ala Pro Glu	Gly Asp Asn Arg Val	Trp Tyr Met Asp Gly	Tyr
	230	235	240
His Asn Asn Arg	Phe Val Arg Glu Tyr	Lys Ser Met Val Asp	Phe
	245	250	255
Met Asn Thr Asp	Asn Phe Thr Ser His	Arg Leu Pro His Pro	Trp
	260	265	270
Ser Gly Thr Gly	Gln Val Val Tyr Asn	Gly Ser Ile Tyr Phe	Asn
	275	280	285
Lys Phe Gln Ser	His Ile Ile Ile Arg	Phe Asp Leu Lys Thr	Glu
	290	295	300
Thr Ile Leu Lys	Thr Arg Ser Leu Asp	Tyr Ala Gly Tyr Asn	Asn
	305	310	315
Met Tyr His Tyr	Ala Trp Gly Gly His	Ser Asp Ile Asp Leu	Met
	320	325	330
Val Asp Glu Asn	Gly Leu Trp Ala Val	Tyr Ala Thr Asn Gln	Asn
	335	340	345
Ala Gly Asn Ile	Val Ile Ser Lys Leu	Asp Pro Val Ser Leu	Gln
	350	355	360
Ile Leu Gln Thr	Trp Asn Thr Ser Tyr	Pro Lys Arg Ser Ala	Gly
	365	370	375
Glu Ala Phe Ile	Ile Cys Gly Thr Leu	Tyr Val Thr Asn Gly	Tyr
	380	385	390
Ser Gly Gly Thr	Lys Val His Tyr Ala	Tyr Gln Thr Asn Ala	Ser
	395	400	405
Thr Tyr Glu Tyr	Ile Asp Ile Pro Phe	Gln Asn Lys Tyr Ser	His
	410	415	420
Ile Ser Met Leu	Asp Tyr Asn Pro Lys	Asp Arg Ala Leu Tyr	Ala
	425	430	435
Trp Asn Asn Gly	His Gln Thr Leu Tyr	Asn Val Thr Leu Phe	His
	440	445	450
Val Ile Arg Ser	Asp Glu Leu		
	455		

<210> 19

<211> 369

<212> PRT

<213> Bos taurus

<300>

<308> g415939

<400> 19

Met	Leu	Leu	Leu	Pro	Leu	Ser	Val	Leu	Leu	Leu	Leu	Thr	Gln	Pro	1	5	10	15
Trp	Arg	Ser	Leu	Gly	Ala	Glu	Met	Lys	Ile	Tyr	Ser	Gln	Lys	Thr	20	25	30	
Met	Ala	Asn	Ala	Cys	Thr	Leu	Val	Met	Cys	Ser	Pro	Pro	Glu	Asp	35	40	45	
Gly	Leu	Pro	Gly	Arg	Asp	Gly	Arg	Asp	Gly	Arg	Glu	Gly	Pro	Arg	50	55	60	
Gly	Glu	Lys	Gly	Asp	Pro	Gly	Ser	Pro	Gly	Pro	Ala	Gly	Arg	Ala	65	70	75	
Gly	Met	Pro	Gly	Pro	Ala	Gly	Pro	Ile	Gly	Leu	Lys	Gly	Asp	Asn	80	85	90	
Gly	Ser	Ala	Gly	Glu	Pro	Gly	Pro	Lys	Gly	Asp	Thr	Gly	Pro	Pro	95	100	105	
Gly	Pro	Pro	Gly	Met	Pro	Gly	Pro	Ala	Gly	Arg	Glu	Gly	Pro	Ser	110	115	120	
Gly	Lys	Gln	Gly	Ser	Met	Gly	Pro	Pro	Gly	Thr	Pro	Gly	Pro	Lys	125	130	135	
Gly	Asp	Thr	Gly	Pro	Lys	Gly	Gly	Val	Gly	Ala	Pro	Gly	Ile	Gln	140	145	150	
Gly	Ser	Pro	Gly	Pro	Ala	Gly	Leu	Lys	Gly	Glu	Arg	Gly	Ala	Pro	155	160	165	
Gly	Glu	Pro	Gly	Ala	Pro	Gly	Arg	Ala	Gly	Ala	Pro	Gly	Pro	Ala	170	175	180	
Gly	Ala	Ile	Gly	Pro	Gln	Gly	Pro	Ser	Gly	Ala	Arg	Gly	Pro	Pro	185	190	195	
Gly	Leu	Lys	Gly	Asp	Arg	Gly	Thr	Pro	Gly	Glu	Arg	Gly	Ala	Lys	200	205	210	
Gly	Glu	Ser	Gly	Leu	Ala	Glu	Val	Asn	Ala	Leu	Arg	Gln	Arg	Val	215	220	225	
Gly	Ile	Leu	Glu	Gly	Gln	Leu	Gln	Arg	Leu	Gln	Asn	Ala	Phe	Ser	230	235	240	
Gln	Tyr	Lys	Lys	Ala	Met	Leu	Phe	Pro	Asn	Gly	Arg	Ser	Val	Gly	245	250	255	
Glu	Lys	Ile	Phe	Lys	Thr	Val	Gly	Ser	Glu	Lys	Thr	Phe	Gln	Asp	260	265	270	
Ala	Gln	Gln	Ile	Cys	Thr	Gln	Ala	Gly	Gly	Gln	Leu	Pro	Ser	Pro	275	280	285	
Arg	Ser	Gly	Ala	Glu	Asn	Glu	Ala	Leu	Thr	Gln	Leu	Ala	Thr	Ala	290	295	300	
Gln	Asn	Lys	Ala	Ala	Phe	Leu	Ser	Met	Ser	Asp	Thr	Arg	Lys	Glu	305	310	315	
Gly	Thr	Phe	Ile	Tyr	Pro	Thr	Gly	Glu	Pro	Leu	Val	Tyr	Ser	Asn	320	325	330	
Trp	Ala	Pro	Gln	Glu	Pro	Asn	Asn	Asp	Gly	Gly	Ser	Glu	Asn	Cys	335	340	345	
Val	Glu	Ile	Phe	Pro	Asn	Gly	Lys	Trp	Asn	Asp	Lys	Val	Cys	Gly	350	355	360	
Glu	Gln	Arg	Leu	Val	Ile	Cys	Glu	Phe							365			

<210> 20
 <211> 313
 <212> PRT
 <213> Mus musculus

<300>
 <308> g3357909

<400> 20

Met	Thr	Gln	Leu	Gly	Phe	Leu	Leu	Phe	Ile	Met	Val	Ala	Thr	Arg					
1				5					10					15					
Gly	Cys	Ser	Ala	Ala	Glu	Glu	Asn	Leu	Asp	Thr	Asn	Arg	Trp	Gly					
				20					25					30					
Asn	Ser	Phe	Phe	Ser	Ser	Leu	Pro	Arg	Ser	Cys	Lys	Glu	Ile	Lys					
				35					40					45					
Gln	Glu	His	Thr	Lys	Ala	Gln	Asp	Gly	Leu	Tyr	Phe	Leu	Arg	Thr					
				50					55					60					
Lys	Asn	Gly	Val	Ile	Tyr	Gln	Thr	Phe	Cys	Asp	Met	Thr	Thr	Ala					
				65					70					75					
Gly	Gly	Gly	Trp	Thr	Leu	Val	Ala	Ser	Val	His	Glu	Asn	Asn	Met					
				80					85					90					
Arg	Gly	Lys	Cys	Thr	Val	Gly	Asp	Arg	Trp	Ser	Ser	Gln	Gln	Gly					
				95					100					105					
Asn	Arg	Ala	Asp	Tyr	Pro	Glu	Gly	Asp	Gly	Asn	Trp	Ala	Asn	Tyr					
				110					115					120					
Asn	Thr	Phe	Gly	Ser	Ala	Glu	Ala	Ala	Thr	Ser	Asp	Asp	Tyr	Lys					
				125					130					135					
Asn	Pro	Gly	Tyr	Phe	Asp	Ile	Gln	Ala	Glu	Asn	Leu	Gly	Ile	Trp					
				140					145					150					
His	Val	Pro	Asn	Lys	Ser	Pro	Leu	His	Asn	Trp	Arg	Lys	Ser	Ser					
				155					160					165					
Leu	Leu	Arg	Tyr	Arg	Thr	Phe	Thr	Gly	Phe	Leu	Gln	His	Leu	Gly					
				170					175					180					
His	Asn	Leu	Phe	Gly	Leu	Tyr	Lys	Lys	Tyr	Pro	Val	Lys	Tyr	Gly					
				185					190					195					
Glu	Gly	Lys	Cys	Trp	Thr	Asp	Asn	Gly	Pro	Ala	Leu	Pro	Val	Val					
				200					205					210					
Tyr	Asp	Phe	Gly	Asp	Ala	Arg	Lys	Thr	Ala	Ser	Tyr	Tyr	Ser	Pro					
				215					220					225					
Ser	Gly	Gln	Arg	Glu	Phe	Thr	Ala	Gly	Tyr	Val	Gln	Phe	Arg	Val					
				230					235					240					
Phe	Asn	Asn	Glu	Arg	Ala	Ala	Ser	Ala	Leu	Cys	Ala	Gly	Val	Arg					
				245					250					255					
Val	Thr	Gly	Cys	Asn	Thr	Glu	His	His	Cys	Ile	Gly	Gly	Gly	Gly					
				260					265					270					
Phe	Phe	Pro	Glu	Gly	Asn	Pro	Val	Gln	Cys	Gly	Asp	Phe	Ala	Ser					
				275					280					285					
Phe	Asp	Trp	Asp	Gly	Tyr	Gly	Thr	His	Asn	Gly	Tyr	Ser	Ser	Ser					
				290					295					300					
Arg	Lys	Ile	Thr	Glu	Ala	Ala	Val	Leu	Leu	Phe	Tyr	Arg							
				305					310										